

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 21, 2003, 12:05:43 ; Search time 455 Seconds
(without alignments)
10369.091 Million cell updates/sec

Title: US-08-991-862-16
Perfect score: 2095
Sequence: 1 cgcagcgacagcattgac.....ataaattgtcattctt 2095

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2093.4	99.9	2095	20	AAV82825
2	2093.4	99.9	2124	14	AAQ56794
3	2093.4	99.9	2198	14	AAQ49052
4	2021.8	96.5	2135	24	AAQ22850
5	2014	96.1	2152	24	ABK64817
6	2014	96.1	2178	24	ABK63501
7	2014	96.1	2432	21	AAQ78180
8	1756.6	83.8	1779	12	AAQ14339
9	1271.2	60.7	1630	22	AAH16370

10	1206.4	57.6	2137	24	AAD32849	Mouse granulin/epi
11	1204.8	57.5	2137	20	AAV82824	Mouse GP88 autocr
12	1142.6	54.5	1767	12	AAQ14338	Rat epithelin prec
13	1107.4	52.9	1767	12	AAQ14340	Mouse epithelin pr
14	483.8	23.1	561	21	AAQ69779	Human ovarian carc
15	483.8	23.1	561	21	AAQ69779	Human ovarian carc
16	424	20.2	757	22	AAH07141	Ovarian carcinoma
17	396.8	18.9	539	12	AAQ14952	Human CDNA clone (
18	381.2	18.2	561	21	AAQ14952	Bovine epithelin p
19	381.2	18.2	561	21	AAQ69780	Human ovarian carc
20	339.2	16.2	439	16	AAQ22115	Ovarian carcinoma
21	258	12.3	598	24	AAQ73892	Human gene signatu
22	228.8	10.9	233	22	AAQ18681	Bovine embryonic g
23	214.6	10.2	289	24	AAQ57741	Human brain expres
24	206.6	9.9	565	22	AAQ53492	Human colon cancer
25	197.8	9.4	336	22	AAQ53492	Murine transport a
26	197.8	9.4	336	22	AAQ53492	Human ovarian PCR-
27	195.6	9.3	390	22	AAQ05895	Human ovarian tumo
28	139	6.6	561	21	AAQ69780	Human ovarian carc
29	139	6.6	561	24	AAQ72674	Ovarian carcinoma
30	107.6	5.1	250	24	AAQ72674	Human ovarian carc
31	82	3.9	199	14	AAQ49051	Probe (grnA) used
32	72.6	3.5	341	12	AAQ14953	Chicken epithelin
33	65.4	3.1	430	22	AAQ182981	Human polynucleoti
34	60	2.9	60	24	AAQ41775	Human polynucleoti
35	57	2.7	177	22	AAQ15045	Oryctolagus cunicu
36	55.6	2.7	108	24	AAQ15045	Human ovarian carc
37	50.2	2.4	51	21	AAQ15693	Human secreted pro
38	44.2	2.1	65	24	AAQ56600	Mouse secreted tran
39	43.4	2.1	1806	21	AAQ50102	Human Zntf2 consen
40	43	2.1	2608	22	AAQ98385	Human CDNA clone B
41	43	2.1	10732	23	AAQ10594	Gene encoding a su
42	41.6	2.0	3729	23	AAQ94337	DNA encoding novel
43	40	1.9	1661	24	AAQ34651	Human CDNA for nov
44	40	1.9	1824	23	AAQ81488	DNA encoding novel
45	40	1.9	2243	22	AAQ08657	Human extensin hom

ALIGNMENTS

RESULT 1	AAV82825	standard; CDNA; 2095 BP.
ID	AAV82825	
XX	AAV82825	
AC	AAV82825	
XX	15-MAR-1999	(first entry)
DT	15-MAR-1999	
XX	Human GP88	autocrine growth factor CDNA.
DE	Human GP88	autocrine growth factor CDNA.
XX	GP88;	granulin; epithelin; human; growth factor; autocrine; tumour;
KW	cancer; vital	infection; antagonistic; therapy; diagnosis; ss.
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	Key	Location/Qualifiers
FT	CDs	13.1794
FT		/tag= a
PN	W09852607-A1.	
XX	26-NOV-1998.	
PD	26-NOV-1998.	
XX	22-MAY-1998;	98WO-US10555.
PF	22-MAY-1998;	98WO-US10555.
XX	16-DEC-1997;	97US-0991862.
PR	23-MAY-1997;	97US-0991862.
XX	(SERR)	SERRERO G.
PA	(SERR)	SERRERO G.
XX	Serrero G;	
PI	Serrero G;	
XX	Serrero G;	

DR WPI: 1999-045276/04.
DR P-PSDB: AAM85475.

Composition containing antagonist of growth factor GP88 - useful for
treating cancer and viral diseases and also for diagnosing disease
from altered GP88 expression

XX PS Disclosure: Fig 9A; 86pp; English.

CC This human cDNA sequence includes a coding region for GP88 (see
CC AAM85474), an 88 kDa glycoprotein autocrine growth factor and
CC epithelial/granulin precursor that is expressed in a tightly
CC regulated manner in normal cells, is overexpressed and unregulated
CC in highly tumorigenic cells derived from normal cells, and which
CC acts as a stringently required growth stimulator for the
CC tumorigenic cells. Inhibition of GP88 expression or action in the
CC properties of the overproducing cells. Antagonists to GP88 are
CC used to treat diseases associated with increased expression of
CC GP88, particularly cancer but also viral infections. Fragments of
CC GP88 are used to raise specific antibodies (used as antagonists,
CC as diagnostic reagents and for delivering toxins or other
CC compounds to GP88-expressing cells) and to screen for antibodies.
CC Antisense oligonucleotides can also be used as antagonists.
CC Methods are provided for diagnosing disease, or determining
CC susceptibility to disease, resulting from altered GP88 activity.

XX Sequence 2095 BP; 364 A; 681 C; 625 G; 425 T; 0 other;

Query Match 99.9%; Score 2093.4; DB 20; Length 2095;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2094; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCAGGACAGCATGTGACCTGTGAGCTGGTGCCTTAACAGACAGGGCTGTGCT 60
DB 1 CGCAGGACAGCATGTGACCTGTGAGCTGGTGCCTTAACAGACAGGGCTGTGCT 60
QY 61 GGAACGGGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 61 GGAACGGGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 121 GCCAGCTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 121 GCCAGCTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 GTGGTGGCCCTGTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 181 GTGGTGGCCCTGTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 241 GTCTGAGGACTTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 241 GTCTGAGGACTTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 CACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 CACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 GGTAAACAATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420
DB 361 GGTAAACAATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420
QY 421 TCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 421 TCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 TGCCTGGAAG 540
DB 481 TGCCTGGAAG 540
QY 541 CGCTGATAC 600
DB 541 CGCTGATAC 600

QY 601 AACAGGACAGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 AACAGGACAGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 GATGTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 661 GATGTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 721 GCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 721 GCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 CAGAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 781 CAGAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 841 CACACAGTGGGAGTGTGAATGTGACATGAGAGTGTGCTGCTGCTGCTGCTGCTGCT 900
DB 841 CACACAGTGGGAGTGTGAATGTGACATGAGAGTGTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 TCCCGTCTACAGTGGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 960
DB 901 TCCCGTCTACAGTGGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 960
QY 961 GACCAATACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 961 GACCAATACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 CAGGGGCCCCACAGTGGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1080
DB 1021 CAGGGGCCCCACAGTGGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1080
QY 1081 CCACAAGCTTGAAGAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1081 CCACAAGCTTGAAGAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 ACCCTGTCACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 1141 ACCCTGTCACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1201 TGCCTGGACACACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1201 TGCCTGGACACACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
QY 1261 CAGCAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 CAGCAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 TCCCAACCCAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1321 TCCCAACCCAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1381 TGCCTGAGCAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1440
DB 1381 TGCCTGAGCAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1440
QY 1441 GATCCGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1441 GATCCGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
QY 1501 AAGGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
DB 1501 AAGGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1561 AAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1620
DB 1561 AAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1620
QY 1621 AACCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
DB 1621 AACCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
QY 1681 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740

Db	1681	CACCTGCTGCTGCTGCTGCTTCCGCTGCGACGACGGGGTACCAAGTGTTCGCGAGGGAG	1740
Qy	1741	GGCCCGCGCTGGGAGCGCCCTTTGAGGGAGCCAGCCCTTGAGACAGCTGCTGAGGGACA	1800
Db	1741	GGCCCGCGCTGGGAGCGCCCTTTGAGGGAGCCAGCCCTTGAGACAGCTGCTGAGGGACA	1800
Qy	1801	GTACTGAAAGACTCTGCAAGCCCTGGGACCCCACTCGGAGGGGTGCCCTCTAGGCTC	1860
Db	1801	GTACTGAAAGACTCTGCAAGCCCTGGGACCCCACTCGGAGGGGTGCCCTCTAGGCTC	1860
Qy	1861	CCTAGACCTCCGCCCAATCTCCCTGGACCCCATCTGAGCTCCCAATCACCAT	1920
Db	1861	CCTAGACCTCCGCCCAATCTCCCTGGACCCCATCTGAGCTCCCAATCACCAT	1920
Qy	1921	GGGAGGTGGGGGCTCAATCTAAAGCCCTTCCCTGTCAGAAAGGGGTTGAGGCAAAACCC	1980
Db	1921	GGGAGGTGGGGGCTCAATCTAAAGCCCTTCCCTGTCAGAAAGGGGTTGAGGCAAAACCC	1980
Qy	1981	ATTACAAAGCTGCGATCCCTCCCGCTTCACTGAGGACCCCTGGCCAGGTCTTCCCTTA	2040
Db	1981	ATTACAAAGCTGCGATCCCTCCCGCTTCACTGAGGACCCCTGGCCAGGTCTTCCCTTA	2040
Qy	2041	TCCACAGGGGCTGTTGTGTGGTGGGTGCTTCAATAAGTTGTCATTCTT	2095
Db	2041	TCCACAGGGGCTGTTGTGTGGTGGGTGCTTCAATAAGTTGTCATTCTT	2095
RESULT 2			
AA056794			
ID	AA056794 standard; DNA; 2124 BP.		
XX	AA056794;		
AC			
XX			
DT	22-APR-1994 (first entry)		
XX			
DE	Granulin coding sequence.		
KW	Granulin; keratinocytes; wound healing; inhibition; peptide;		
KW	granulocytes; leucocytes; sg.		
OS	Homo sapiens.		
XX			
FT	Key	Location/Qualifiers	
FT	misc_difference	1379..1381	
FT		/*tag= a	
FT		/trans_except= Arg encodes Valine.	
FT	misc_difference	1640..1642	
FT		/*tag= b	
FT		/trans_except= CAG encodes Glycine.	
XX	W09315195-A.		
XX			
XX	05-AUG-1993.		
XX			
XX	28-FEB-1992; 92WO-CA00089.		
XX			
XX	03-FEB-1992; 92US-0829233.		
XX			
PA	(SOLO/) SOLOMON S.		
XX			
PT	Solomon S;		
XX			
XX	WPI; 1993-320328/40.		
DR	P-PSDB; AAR48673.		
XX			
PT	New cysteine rich granulin peptide(s) from leucocyte(s) - are		
PT	keratinocyte inhibitors useful topically for wound healing		
XX			
PS	Disclosure; Figure 4c; 53pp; English.		
XX			
CC	The granulin inhibits keratinocytes and is useful in formulations		
CC	for promoting the healing of wounds.		

XX	Sequence	2124 BP; 383 A; 685 C; 630 G; 426 T; 0 other:
SQL	99.9%; Score 2093.4; DB 14; Length 2124; Best Local Similarity 100.0%; Pred. No. 0; Matches 2094; Conservative 0; Mismatches 1; Indels 0; Gaps 0.	
Query Match		
1	CGCAGGACAGACCATGTGACCCCTGCTGAGCTGGGGGCGCTTAACAGACAGGCTGTGGCT	60
Db	14 CGCAGGACAGACCATGTGAGACCCCTGGAGCTGGTGGCTTAACAGACAGGCTGTGGCT	73
QY	61 GGAAGCGGGTGGCCAGATAGTCAATTCTCCCTGTGGCTGTGCTTGGACCCCGGAGCA	120
Db	74 GGAAGCGGGTGGCCAGATAGTCAATTCTCCCTGTGGCTGTGCTTGGACCCCGGAGCA	133
QY	121 GGCAGCTACAGTGTGCTGCCGCTCCCTTTCGAGCAAAATGGCCCAACACACTGGAGCAGGAT	180
Db	134 GGCAGCTACAGTGTGCTGCCGCTCCCTTTCGAGCAAAATGGCCCAACACACTGGAGCAGGAT	193
QY	181 CTGGGTGGCCCTGCGCCAGGTGATGAGCCACACTGCTGTGCCGGCCACTCTGCATCTTTAAC	240
Db	194 CTGGGTGGCCCTGCGCCAGGTGATGAGCCACACTGCTGTGCCGGCCACTCTGCATCTTTAAC	253
QY	241 GTCCTAGGAGACTTCCAGTTGTGCTGCCCTTCCAGAGCGCGTGGCATGCGGGAGTGGCCAT	300
Db	254 GTCCTAGGAGACTTCCAGTTGTGCTGCCCTTCCAGAGCGCGTGGCATGCGGGAGTGGCCAT	313
QY	301 CACTGTGCGCCACAGGGGCTTCCACTCTCAGTGTGAGAGGAGGCGATGCTGCTCCAAAGATCA	360
Db	314 CACTGTGCGCCACAGGGGCTTCCACTCTCAGTGTGAGAGGAGGCGATGCTGCTCCAAAGATCA	373
QY	361 GGTAAACACTCCGTGGGGTCCATCCAGTCCCTGATATGTCAGTTGCAATGCCCGGACTTC	420
Db	374 GGTAAACACTCCGTGGGGTCCATCCAGTCCCTGATATGTCAGTTGCAATGCCCGGACTTC	433
QY	421 TCCAGTGTGTGTATGTGTCATGGCTCTCTGGGGTGTCTGCCCATGCCCCAGGCTTCC	480
Db	434 TCCAGTGTGTGTATGTGTCATGGCTCTCTGGGGTGTCTGCCCATGCCCCAGGCTTCC	493
QY	481 TCCGTGGAAGACAGGGTGTGACGTGCTTCCGACAGGGTCTTTCGGACCTGGGTTCACAC	540
Db	494 TCCGTGGAAGACAGGGTGTGACGTGCTTCCGACAGGGTCTTTCGGACCTGGGTTCACAC	553
QY	541 CGCTGCATCACACCACAGGGACCCACCCCTGGCCAAAGATGCTCCTGCCAGAGACT	600
Db	554 CGCTGCATCACACCACAGGGACCCACCCCTGGCCAAAGATGCTCCTGCCAGAGACT	613
QY	601 AACAGGGCAGTGGCTTGTTCAGCTCGGTGATGTGTCCGGAGCGACGTTCCGGTGCCCT	660
Db	614 AACAGGGCAGTGGCTTGTTCAGCTCGGTGATGTGTCCGGAGCGACGTTCCGGTGCCCT	673
QY	661 GATGGTTCACCGCTGTGAGCGTCCCACTGGGAATATGGTGTGCCCATATGCCCAAC	720
Db	674 GATGGTTCACCGCTGTGAGCGTCCCACTGGGAATATGGTGTGCCCAATGCCCAAC	733
QY	721 GGCACCTGCTGTCCGATACCTGTGACCTCTGCTGCCCAAGACACTGTGTGACCTGATC	780
Db	734 GGCACCTGCTGTCCGATACCTGTGACCTCTGCTGCCCAAGACACTGTGTGACCTGATC	793
QY	781 CAGAGTAACTGCTCTCCAGAGAAAGCTACACAGGACCTCCTCACTAAGTGGCTGGG	840
Db	794 CAGAGTAACTGCTCTCCAGAGAAAGCTACACAGGACCTCCTCACTAAGTGGCTGGG	853
QY	841 CACACAGTGGGGAGTGAATGTGACATGAGAGTGAAGTGGCCAGATGGCATATACCTGC	900
Db	854 CACACAGTGGGGAGTGAATGTGACATGAGAGTGAAGTGGCCAGATGGCATATACCTGC	913
QY	901 TACCGCTACATCGGGGGCTGTGGGGCTCTGCTGCCCTTTACCAAGGCTGTGTGCTGTAG	960
Db	914 TACCGCTACATCGGGGGCTGTGGGGCTCTGCTGCCCTTTACCAAGGCTGTGTGCTGTAG	973
QY	961 GACCAATACACTGTGTGTCGCCGGGGTTTACGTGTGACACGACAGAGGGTACTGTGA	1020

OY	301	CAGTGTGGCCACGGGGGCTTCCACTGTCAGAGCGAGCGGGGAGATCGTCTCCAAAGATCA	360
Db	388	CAGTGTGGCCACGGGGGCTTCCACTGTCAGAGCGAGCGGGGAGATCGTCTCCAAAGATCA	447
OY	361	GGTAACAATCCGTGGGTGCCATCCAGTGCCTGATAGTCAGTTGCAATGCCCCGCAATTC	420
Db	448	GGTAACAATCCGTGGGTGCCATCCAGTGCCTGATAGTCAGTTGCAATGCCCCGCAATTC	507
OY	421	TCCAGTGTGTGTATATGTCGATGGCTCTGTGGGGTGTCTGGCCCCATGCCCCAGGCTTC	480
Db	508	TCCAGTGTGTGTATATGTCGATGGCTCTGTGGGGTGTCTGGCCCCATGCCCCAGGCTTC	567
OY	481	TGCTGTGAAGACAGGGGTGCACTGCTCCGCAAGGATGGCTTCGACCGCTGGATTACACC	540
Db	568	TGCTGTGAAGACAGGGGTGCACTGCTCCGCAAGGATGGCTTCGACCGCTGGATTACACC	627
OY	541	CGCTGCATCACACCCACGGGGCAACCCGCCCTGGCAAGAAGCTCCCTGCCACGAGAGCT	600
Db	628	CGCTGCATCACACCCACGGGGCAACCCGCCCTGGCAAGAAGCTCCCTGCCACGAGAGCT	687
OY	601	AACAGGGCAGTGGCTTGTCCAGCTGGGTATGTGTCCGAGCGACAGGTCCGGGTGCTT	660
Db	688	AACAGGGCAGTGGCTTGTCCAGCTGGGTATGTGTCCGAGCGACAGGTCCGGGTGCTT	747
OY	661	GATGGTTTACGTCGCTGTAGAGCGCCACGATGGGAAGATATGGCTGTGTGCCCAATGCCAAC	720
Db	748	GATGGTTTACTACTGCTGTAGAGCTGCCCAATGGGAATATGGCTGTGTGCCCAATGCCAAC	807
OY	721	GCCACCTGCTGCTCCGATCATCCTGCACCTGCTGCCCCCAAGACACTGTGTGTGACTGTATC	780
Db	808	GCCACCTGCTGCTCCGATCATCCTGCACCTGCTGCCCCCAAGACACTGTGTGTGACTGTATC	867
OY	781	CAGAGTAATGTGCTCTCCAAAGAAACGCTACACGAGACTCCTCACTAAGTGTGCTGGC	840
Db	868	CAGAGTAATGTGCTCTCCAAAGAAACGCTACACGAGACTCCTCACTAAGTGTGCTGGC	927
OY	841	CACACAGTGGGGATGTGAAATGTGACATGAGAGGTGAGCGCCACATGTGACTTAATTC	900
Db	928	CACACAGTGGGGATGTGAAATGTGACATGAGAGGTGAGCGCCACATGTGACTTAATTC	987
OY	901	TGCCGTCTACAGTGGGGGCTGTGGGGCTCTGCCCTTTTACCAGGCTGTGTGCTGTGAG	960
Db	988	TGCCGTCTACAGTGGGGGCTGTGGGGCTCTGCCCTTTTACCAGGCTGTGTGCTGTGAG	1047
OY	961	GACCAATATCACTGCTGTGTCCCGGGGGTTTACTGTGTGACACGAGAAAGGTACTGTGAA	1020
Db	1048	GACCAATATCACTGCTGTGTCCCGGGGGTTTACTGTGTGACACGAGAAAGGTACTGTGAA	1107
OY	1021	CAGGGGGCCACACAGTGTGCTGTGATGAGAAAGGCCCAAGCTACCTCAGCTGTGCCAGAC	1080
Db	1108	CAGGGGGCCACACAGTGTGCTGTGATGAGAAAGGCCCAAGCTACCTCAGCTGTGCCAGAC	1167
OY	1081	CCACAAGCTTGAAGAGAGATGTCCCTGTGATATGTGACGACGCTGTCCCTCCGAT	1140
Db	1168	CCACAAGCTTGAAGAGAGATGTCCCTGTGATATGTGACGACGCTGTCCCTCCGAT	1227
OY	1141	ACCTGTGTCAACTCACGCTGTGGGAGTGGGGTGTGTGCCAATGCCAAGGCTGTCTGC	1200
Db	1228	ACCTGTGTCAACTCACGCTGTGGGAGTGGGGTGTGTGCCAATGCCAAGGCTGTCTGC	1287
OY	1201	TGCTGTGCACACACAGCATGTGTCCCCACAGCGATATACGCTGTGTACTGTAGGGGCAAGTGT	1260
Db	1288	TGCTGTGCACACACAGCATGTGTCCCCACAGCGATATACGCTGTGTACTGTAGGGGCAAGTGT	1347
OY	1261	CAGCGAGGAAGGAGATGCTGTGCTGTGAGCTGTGAGAGATGCTGCCCGCGGGTTCCTTA	1320
Db	1348	CAGCGAGGAAGGAGATGCTGTGCTGTGAGCTGTGAGAGATGCTGCCCGCGGGTTCCTTA	1407
OY	1321	TCCCAACCCAGAGACATGTGGCTGTGTGACACAGACATCAGAGCTGCCCGGATGGGCGGAACCTGC	1380
Db	1408	TCCCAACCCAGAGACATGTGGCTGTGTGACACAGACATCAGAGCTGCCCGGATGGGCGGAACCTGC	1467

OY	1381	TGCCCCAGACAGGGGGAGCTGGGGCTGTGCATCGCCAGTTGGCCCAATGCTGTGTGGCAG	1440
.Db.	1468	TGCCCGAGCCAGGGTGGGAAGCTGGGGCTGTGTGCCAGTTGCCCATGTGTGTGTGTGGAG	1527
OY	1441	GATGCGCAGACACTGTCGCCCGGGCTGGCTTACACCTTGCAAAGTAAGAGCTGATTCCTGGAG	1500
.Db	1528	GATGCCCGACAGACTGCTGCCCCGGCTGGCTTACACCTTGCAAAGTAAGAGCTGATTCCTGGAG	1587
OY	1501	AAGGAAGTGTCTGTGCCAGGCTGGCCACAATTCCGTGGCGCGGTACGCCCTCACGTGGGTGTG	1560
.Db	1588	AAGGAAGTGTCTGTGCCAGGCTGGCCACAATTCCGTGGCGCGGTACGCCCTCACGTGGGTGTG	1647
OY	1561	AAGGACGTGTGATGTGGGGAAGGAACTTCTTGCCATGATTAACCAAGACCTGCTGCCGAGAC	1620
.Db	1648	AAGGACGTGTGATGTGGGGAAGGAACTTCTTGCCATGATTAACCAAGACCTGCTGCCGAGAC	1707
OY	1621	AACCAGCAGAGGCTGGGGCTGCTGTCTCTTACAGCCCAGGGCGTCTGTTGTGTGATCGGCGC	1680
.Db	1708	AACCAGCAGAGGCTGGGGCTGCTGTCTCTTACAGCCCAGGGCGTCTGTTGTGTGATCGGCGC	1767
OY	1681	CACCTGTCTGCTGTGGGCTCCGCTGCGCAGCAGAGGGGTACCAAGTGTTCGCGAGGGAG	1740
.Db	1768	CACCTGTCTGCTGTGGGCTCCGCTGCGCAGCAGAGGGGTACCAAGTGTTCGCGAGGGAG	1827
OY	1741	GCCTCCGCGCTGGGAGCGCCCTTTGAGGGAGCCAGCCTTGAGACAGCTGTGTGAGGGACA	1800
.Db	1828	GCCTCCGCGCTGGGAGCGCCCTTTGAGGGAGCCAGCCTTGAGACAGCTGTGTGAGGGACA	1887
OY	1801	GTACTGAAGACTCTGTACACCCCTCGGGAGCCCACTGTGGAGGGTGGCTTGTCTGACGGCTC	1860
.Db	1888	GTACTGAAGACTCTGTACACCCCTCGGGAGCCCACTGTGGAGGGTGGCTTGTCTGACGGCTC	1947
OY	1861	CCTACACACTCCCTCCCTTAACCAAAATCTCTCTGAGAACCCCAATCTAGCTCCCCATCACCAT	1920
.Db	1948	CCTACACACTCCCTCCCTTAACCAAAATCTCTCTGAGAACCCCAATCTAGCTCCCCATCACCAT	2007
OY	1921	GGGAGGTGGGGCTGTCAATCTAAGGCCCTTCCCTGTCTGAGAGGGGGTGTGAGCAAAAGCCC	1980
.Db	2008	GGGAGGTGGGGCTGTCAATCTAAGGCCCTTCCCTGTCTGAGAGGGGGTGTGAGCAAAAGCCC	2067
OY	1981	ATTACAGGTGCATCCCTCCCTGTCTGAGTAGGGACCTGTGGGAGAGTGTTCCTTA	2040
.Db	2068	ATTACAGGTGCATCCCTCCCTGTCTGAGTAGGGACCTGTGGGAGAGTGTTCCTTA	2127
OY	2041	TCCACAGGGGGTGTGTGTGTGGTGTGTCTTCATAATAATTTGTCACTTCTT	2095
.Db	2128	TCCACAGGGGGTGTGTGTGTGGTGTGTCTTCATAATAATTTGTCACTTCTT	2182
RESULT 4			
AAD32850			
ID	AAD32850	standard; CDNA: 2155 BP.	
XX	AAD32850;		
AC			
XX			
DT	01-JUL-2002	(first entry)	
XX			
DE	Human granulin/epithelin precursor (GP88) cDNA.		
XX			
KM	Human; granul ⁿ precursor; GP88; cytosolic; tumorigenicity; tamoxifen		
KW	antineoplastic; antioestrogen therapy; skin cancer; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	misc_feature	1..374	
FT		/tag= a	
FT		/note= "This region is cloned in the antisense	
FT		orientation in pcDNA3 mammalian expression vector"	
FT	CDS	13..1794	
FT		/tag= b	
FT		/product= "Human GP88 protein"	
FT		/transl_except= (pos:829..831, aa:TYR)	

Db	1501	AAGGAATGGGCTCTGTGCCAGCCTGGCACACTTCTGTGGCCGTGAAGCCCTACGTGGGTGTG	1560
Qy	1501		
Db	1501	AAGGACCTGGAGTGTGGGGGAAGACACCTTCTGCGCATGATTAACCAAGCTGCTGCCGAGAC	1620
Qy	1501		
Db	1561	AAGGACCTGGAGTGTGGGGGAAGACACTTCTGCGCATGATTAACCAAGCTGCTGCCGAGAC	1620
Qy	1621	AACCGAAGGAGGCTGGGGCTCTGTGCCCTACGGCCAGAGGGGTCTGTTGGCTGATGAGGAGC	1680
Db	1621	AACCGAAGGAGGCTGGGGCTCTGTGCCCTACGGCCAGAGGGGTCTGTTGGCTGATGAGGAGC	1680
Qy	1681	CACGTGCTGTCTGTGGTGGCTTCCCTCTGCGACGAGGAGGGATACCAAGTGTGGCGAGGAG	1740
Db	1681	CACGTGCTGTCTGTGGTGGCTTCCCTCTGCGACGAGGAGGGATACCAAGTGTGGCGAGGAG	1740
Qy	1741	GCCCCGGGCTGGGACGCCCCCTTTGAGGAGACCCAGCCTTGAAGACGCTGCTGTGAAGGACA	1800
Db	1741	GCCCCGGGCTGGGACGCCCCCTTTGAGGAGACCCAGCCTTGAAGACGCTGCTGTGAAGGACA	1800
Qy	1801	-----	1800
Db	1801	GTACTGAAGACTGTGCAGCCCTCGGGAGCCACACTGCGGAGGGTGGCCCTGTGTCANAGCCTC	1860
Qy	1801	GTACTGAAGACTGTGCAGCCCTCGGGAGCCACACTGCGGAGGGTGGCCCTGTGTCAGGCTC	1860
Db	1861	GTACTGGAAGACTGTGCAGCCCTCGGGAGCCACACTGCGGAGGGTGGCCCTGTGTCAGGCTC	1920
Qy	1861	CCTGACACCTCCCTCTAACCAAAATTCCTCCCTGGACCCCATTCCTGAGCTCCCATCACCAT	1920
Db	1921	CCTGACACCTCCCTCTAACCAAAATTCCTCCCTGGACCCCATTCCTGAGCTCCCATCACCAT	1980
Qy	1921	GGGAGGTGGGGCCTCAATCTAAGGCCCTTCCCTGTGACAGAGGGGGTTGAGGCAAAAGCCC	1980
Db	1981	GGGAGGTGGGGCCTCAATCTAAGGCCCTTCCCTGTGACAGAGGGGGTTGAGGCAAAAGCCC	2040
Qy	1981	ATTACAGCTGTGCATGCCCTCCCTCCCTTTCAGTGGAGACCTGTGGCCAGAGGCTTTCCTTA	2040
Db	2041	ATTACAGCTGTGCATGCCCTCCCTCCCTTTCAGTGGAGACCTGTGGCCAGAGGCTTTCCTTA	2100
Qy	2041	TCCACAGAGGGGTGTTGTGTGTGGTGTGCTTTCATATAAGTTTGTCACTTCTT	2095
Db	2101	TCCACAGAGGGGTGTTGTGTGTGGTGTGCTTTCATATAAGTTTGTCACTTCTT	2155
RESULT 5			
ABK64817			
ID	ABK64817	standard; DNA; 2152 BP.	
XX	ABK64817;		
AC			
XX			
DT	18-JUN-2002	(first entry)	
XX			
DE		Human benign prostatic hyperplasia gene #712.	
XX			
XX		Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.	
OS		Homo sapiens.	
XX			
PN	WO200212440-A2.		
XX			
PD	14-FEB-2002.		
XX			
PF	07-AUG-2001; 2001WO-US24708.		
XX			
PR	07-AUG-2000; 2000US-223323P.		
PR	05-JUN-2001; 2001US-0873319.		
XX			
PA	(GENE-) GENE LOGIC INC.		
XX	(NISB) JAPAN TOBACCO INC.		
PI	Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;		
XX			
DR	WPI; 2002-257476/30.		

Query Match	Best Local Similarity	96.1%	Score 2014;	DB 24;	Length 2152;
Matches 2045;	Conservative	0;	Pred. No. 0;	Mismatches 15;	Indels 2;
Gaps					
1	CGCAGGACACCATGTGGACCCCTGGTGACCTGGTGCGCTTAAACAGCAGGCGTGGGCT	60			
29	CGCAGGACACCATGTGGACCCCTGGTGACCTGGTGCGCTTAAACAGCAGGCGTGGGCT	88			
61	GGAGCGCGGTGCCAGATAGTCAGTTCTCCCTGTGGCCCTGCTGACCCCGGAGGA	120			
89	GGAGCGCGGTGCCAGATAGTCAGTTCTCCCTGTGGCCCTGCTGACCCCGGAGGA	148			
121	GGCAGCTACAGCTGCTGCGCGCTCCCTTCTGGACAATGGCCCAACACTGAGCAGCAAT	180			
149	GGCAGCTACAGCTGCTGCGCGCTCCCTTCTGGACAATGGCCCAACACTGAGCAGCAAT	208			
181	CTGGGGGGCGCCCGCCAGGTTGATGACCACTGCTGCGCGGCGACATCCGCATCTTTACC	240			
209	CTGGGGGGCGCCCGCCAGGTTGATGACCACTGCTGCGCGGCGACATCCGCATCTTTACC	268			
241	GTCTCAGGAGCTTCCAGTTGCTGCCCTTCCAGAGGCGCGTGAGCATGCGGAGTGGCAAT	300			
269	GTCTCAGGAGCTTCCAGTTGCTGCCCTTCCAGAGGCGCGTGAGCATGCGGAGTGGCAAT	328			
301	CACCTGTGCCACAGGGGCTTCCACATGACATGACAGAGGGCGATCTGCTTCCAAAGATCA	360			
329	CACCTGTGCCACAGGGGCTTCCACATGACATGACAGAGGGCGATCTGCTTCCAAAGATCA	388			
361	GGTAACAATCCGTGGGTGCTCAATCCAGTCCCTGATAGTACAGTCCAAATGCCGGGACTTC	420			
389	GGTAACAATCCGTGGGTGCTCAATCCAGTCCCTGATAGTACAGTCCAAATGCCGGGACTTC	448			
421	TCCAGCTGCTGTTATAGTGCATGGCTCTGGGGGTGCTGCCCATATGCCAGGCTTCC	480			
449	TCCAGCTGCTGTTATAGTGCATGGCTCTGGGGGTGCTGCCCATATGCCAGGCTTCC	508			
481	TGCTGTGAAGACAGGGTGCATGCTGCTCCGACAGTGGTCTTTCGACACTGGTTACACAC	540			
509	TGCTGTGAAGACAGGGTGCATGCTGCTCCGACAGTGGTCTTTCGACACTGGTTACACAC	568			

Dd	1649	AACGCAAGAGGGCTGGGGCTCTGTCCCTTACCAGCGCAGGCGTCGTGTGTCTCATATGGGC	1708
Oy	1681	CATGCTGTCTCTGTGCTTCCGCTCGCACGACGAGGGGTACCAAGTTTGGCAGGGG	1744
Dd	1709	CATGCTGTCTCTGTGCTTCCGCTCGCACGAGCGAGGGGTACCAAGTTTGGCAGGGG	1766
Oy	1741	GCCCCGGGCTGGGACGCCCTTTTGAGGGAGCCAGCTTTAGACAGCTGTGTGAGGACA	1800
Dd	1769	GCCCCGGGCTGGGACGCCCTTTTGAGGGAGCCAGCTTTAGACAGCTGTGTGAGGACA	1828
Oy	1801	GTACTGAAGACTTGTGACGCCCTCGGAGACCCCACTGAGAGGGGCTGTGCTCAGGCTC	1866
Dd	1829	GTACTGAAGACTTGTGAGCCCTCGGAGACCCCACTGAGAGGGGCTGTGCTCAGGCTC	1888
Oy	1861	CCTAGCAGCTCCGCCCTTAACCAAATTCTCCCTGAGCCCAATTCGTAGCTGCCCATACAT	1920
Dd	1889	CCTAGCAGCTCCGCCCTTAACCAAATTCTCCCTGAGCCCAATTCGTAGCTGCCCATACAT	1948
Oy	1921	GGAGGTGGGGCCCTCAATCTAAGGCCCTTCCCTGTACAGAAGGGGTTGAGCAAAAGC-	1979
Dd	1949	GGAGGTGGGGCCCTCAATCTAAGGCCCTTCCCTGTACAGAAGGGGTTGAGCAAAAGC-	2007
Oy	1980	CATTACAGCTGCCATATCCCCTCCGTTTCAGTGGAGACCTGTGGCCAGAGTCTTTCCCT	2039
Dd	2008	CATTACAGCTGCCATATCCCCTCCGTTTCAGTGGAGACCTGTGGCCAGAGTCTTTCCCT	2067
Oy	2040	ATCCACAGGGGTGTGTGTGT 2061	
Dd	2068	ATCCACAGGGGTGTGTGTGT 2089	
 RESULT 6 ABK83501			
ID	ABK83501	standard; cDNA; 2178 bp.	
AC	XX	ABK83501;	
DE	XX	14-AUG-2002 (first entry)	
KW	XX	Human cDNA differentially expressed in granulocytic cells #72.	
KM	XX	Human; ss; granulocytic cell; DNA chip; bacterial infection;	
KW	XX	viral infection; parasitic infection; protozoal infection;	
KM	XX	rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;	
KW	XX	cardiac reperfusion injury; renal reperfusion injury; AIDS;	
KM	XX	Trohn's disease; ulcerative colitis; periodontal disease;	
KW	XX	granulocyte activation; chronic inflammation; allergy.	
OS	XX	Homo sapiens.	
XX	PN	WO200228999-A2.	
XX	PD	11-APR-2002.	
XX	PF	03-OCT-2001; 2001WO-US30821.	
XX	PR	03-OCT-2000; 2000US-237189P.	
XX	PA	(GENE-) GENE LOGIC INC.	
XX	PJ	Beazer-Barclay Y, Weisman SM, Yamaga S, Vockley J;	
XX	DR	WPI; 2002-435328/46.	
PT	XX	Detecting granulocyte activation by detecting differential expression	
PT	XX	of genes associated with granulocyte activation, which serves as	
PT	XX	diagnostic markers that is useful for monitoring disease states and	
PT	XX	drug toxicity	
PS	XX	Claim 1; SEQ ID No. 72; 11Apr. English	

XX The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by CC DNA chip analysis as given in the specification, and comparing CC the expression level to an expression level in an unactivated CC CC, where differential expression of Gs is indicative of GCA. CC Also included are modulating (M2) Gs by contacting Gs with an agent CC that alters the expression of at least one gene in Gs; (2) screening (M3) CC for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease using the CC gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease, by detecting the CC level of expression in a sample of the tissue of gene(s) from Gs, where CC the level of expression of the gene is indicative of inflammation; CC (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen CC or sterile inflammatory disease, by contacting a tissue having CC inflammation with an agent that modulates the expression of gene(s) CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for CC modulating Gs; M3 is useful for screening an agent capable of modulating CC GCA preferably in an inflammation in a tissue; M4 is useful for CC detecting an inflammation (especially chronic) in a tissue, an allergic CC response in a subject, exposure of a subject to a pathogen or sterile CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis, CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal CC reperfusion injury, ARDS, adult respiratory distress syndrome, CC inflammatory bowel disease, Crohn's disease, ulcerative colitis, CC periodontal disease; also bacterial infection, viral infection, CC parasitic infection, protozoal infection, fungal infection and M5 is CC useful for treating one of the above conditions. The present CC sequence represents a gene differentially expressed in granulocytes. CC Note: The sequence data for this patent did not form part CC of the printed specification, but was obtained in electronic CC format directly from WIPO at CC ftp.wipo.int/pub/published_pcl_sequences.

XX Sequence 2178 BP; 401 A; 697 C; 646 G; 434 T; 0 other;

XX Query Match 96.1%; Score 2014; DB 24; Length 2178;

XX Best Local Similarity 99.2%; Pred. No. 0;

XX Matches 2045; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

QY 1 CGCAGCGACACATGTTGACCTGGTGGCTTTACAGCAGGGCTGTGCT 60
DB 51 CGCAGCGACACATGTTGACCTGGTGGCTTTACAGCAGGGCTGTGCT 110
QY 61 GGAACGGGTCGCCAGATGTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 111 GGAACGGGTCGCCAGATGTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 170
QY 121 GCGAGCTACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 171 GCGAGCTACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 230
QY 181 CTGGGTGGCCCTGCGAGTTGATGCCACTGCTGCTGCGGCACTCTGATCTTTAC 240
DB 231 CTGGGTGGCCCTGCGAGTTGATGCCACTGCTGCTGCGGCACTCTGATCTTTAC 290
QY 241 GTCTCAGGAGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 291 GTCTCAGGAGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 350
QY 301 CACTGCTGCCAGCGGGCTTCACTGAGTGCAGACGGGGCATCTGCTTCAAGATCA 360
DB 351 CACTGCTGCCAGCGGGCTTCACTGAGTGCAGACGGGGCATCTGCTTCAAGATCA 410
QY 361 GGTAAACATCCGTTGGTGCATCAGTGCCTGATGATGATGATGATGATGATGAT 420
DB 411 GGTAAACATCCGTTGGTGCATCAGTGCCTGATGATGATGATGATGATGATGAT 470
QY 421 TCCACGTGCTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 480

DB 471 TCCACGTGCTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 530
QY 481 TCCACGTGCTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 531 TCCACGTGCTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 590
QY 541 GGTAAACATCCGTTGGTGCATCAGTGCCTGATGATGATGATGATGATGATGAT 600
DB 591 GGTAAACATCCGTTGGTGCATCAGTGCCTGATGATGATGATGATGATGATGAT 650
QY 601 AACAGGAGTGGCTTGTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 651 AACAGGAGTGGCTTGTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 710
QY 661 GATGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 711 GATGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
QY 721 GCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 771 GCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 830
QY 781 CAGATTAAGTCTTCCAGAGAGAACCTTACAGGACCTTCTCACTAAGCTGCTGCG 840
DB 831 CAGATTAAGTCTTCCAGAGAGAACCTTACAGGACCTTCTCACTAAGCTGCTGCG 890
QY 841 CACACAGTGGGGAGTGAATGTGACATGGAGTGGAGTGGAGTGGAGTGGAGT 900
DB 891 CACACAGTGGGGAGTGAATGTGACATGGAGTGGAGTGGAGTGGAGTGGAGT 950
QY 901 TGCCCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 951 TGCCCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1010
QY 961 GACCAATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 1011 GACCAATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1070
QY 1021 CAGGGGCCCAACAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1071 CAGGGGCCCAACAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1130
QY 1081 CCACAGGCTTGAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1131 CCACAGGCTTGAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1190
QY 1141 ACCCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 1191 ACCCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1250
QY 1201 TGCTGGAGACACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1251 TGCTGGAGACACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1310
QY 1261 CAGCGAGGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1311 CAGCGAGGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1370
QY 1321 TCCACCCCAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1371 TCCACCCCAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1430
QY 1381 TGCCGAGGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1431 TGCCGAGGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1490
QY 1441 GATGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1491 GATGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1550
QY 1501 AAGGAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560

[illegible]

xx	WPI. 2000-587533/55.
DR	P-PsDB; AAB43971.
xx	
PT	Novel isolated nucleic acids comprising sequences encoding peptides
xx	useful for treating or diagnosing e.g. cancer -
PS	Claim 1; Page 1097-1098; 2352pp; English.
xx	
CC	AAC77607 to AAC78448 encode the human cancer associated proteins given
CC	in AAB43398 to ABA44239. The proteins can have activities based on the
CC	tissues and cells the genes are expressed in. Example of activities
CC	include: cytostatic; proliferative; vulnerability; immunomodulator;
CC	antidiabetic; antisthmatic; antirheumatic; antitarrtic;
CC	antiinflammatory; antihypoid; antiallergic; antibacterial; antiviral;
CC	dermatological; neuroprotective; cardiac; thrombolytic; coagulant;
CC	neotropic; vasotropic; antipsoriatic and angiogenic. The
CC	polynucleotides and polypeptides can be used for preventing, treating or
CC	ameliorating medical conditions and diagnosing pathological conditions.
CC	Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC	the present invention may be used to treat immune disorders by activating
CC	or inhibiting the proliferation, differentiation or mobilisation of
CC	immune cells, to treat disorders of haematopoietic cells, autoimmune
CC	disorders, allergic reactions, graft versus host disease and organ
CC	rejection, modulate haemostatic or thrombolytic activity, modulate
CC	inflammation, cancers, cardiovascular disorders, neurological disease and
CC	bacterial or viral infections. The peptides, nucleotides, antibodies,
CC	agonists and antagonists may be also be used in drug screens. AAC78449 to
CC	AAC78457 and AAB44240 represent sequences used in the exemplification of
CC	the present invention.
xx	
SQ	Sequence 2432 BP; 460 A; 764 C; 707 G; 496 T; 5 other:
Query Match	96.1%; Score 2014; DB 21; Length 2432;
Best Local Similarity	99.2%; Pred. No. 0;
Matches 2045; Conservative	0; Mismatches 15; Indels 2; Gaps 2;
OY	1 CGCAGGCGACATCTGGACCCTTGAGACTGGGAGCCCTTAACAGCAGGCTGGGGCT 60
DB	176 CGCAGGCGACCATTTGAACCTTGGAGCTGGGTGGCTTAAACAGCAGGCTGGGGCT 235
OY	61 GGAAAGCGGTGCCAGATGATGTCAGTTTCGCCCTGTGGCCCTGCTGCAGCCCCGAGA 120
DB	236 GGAAGCGGTGCCAGATGATGTCAGTTTCGCCCTGTGGCCCTGCTGCAGCCCCGAGA 295
OY	121 GCCAGCTACAGTGTGCCGCTCCCTTTGGAACAATGGCCCAACAACACTAGCAGGCAT 180
DB	296 GCCAGCTACAGTGTGCCGCTCCCTTTGGAACAATGGCCCAACAACACTAGCAGGCAT 355
OY	181 CTGGGTGGCCCCCTGGCAGATTGATGCCAATGCTCTGGCGGCGACATCCGTGANTTTTACC 240
DB	356 CTGGGTGGCCCCCTGGCAGATTGATGCCAATGCTCTGGCGGCGACATCCGTGANTTTTACC 415
OY	241 GTCTCAGGAGACTTCCAGTTGCTGCCCTTCCAGAGCGCGTGGCATGCGGGAGTGGCAT 300
DB	416 GTCTCAGGAGACTTCCAGTTGCTGCCCTTCCAGAGCGCGTGGCATGCGGGAGTGGCAT 475
OY	301 CACCTCTGCCACGGGGGCTTCCATGCAATGAGACAGCGGCATCTCTGTTCCAAGATCA 360
DB	476 CACCTCTGCCACGGGGGCTTCCATGCAATGAGACAGCGGCATCTCTGTTCCAAGATCA 535
OY	361 GGTAAACAATCCGTTGGGTGCATCCAGTACCCTGTATAGTCAATTGGAATGCCGGACTTC 420
DB	536 GGTAAACAATCCGTTGGGTGCATCCAGTACCCTGTATAGTCAATTGGAATGCCGGACTTC 595
OY	421 TTCACGTCTGTATTATGGTCGATGGCTCTGGGGGTGCTGCCCATGCCAGGCTTCC 480
DB	596 TTCACGTCTGTATTATGGTCGATGGCTCTGGGGGTGCTGCCCATGCCAGGCTTCC 655
OY	481 TGCTGTGAAGAACAGGTCGACATGCTGTCCGACAGGCTCTTGTGGAGACTGGTTACACC 540
DB	656 TGCTGTGAAGAACAGGTCGACATGCTGTCCGACAGGCTCTTGTGGAGACTGGTTACACC 715

QY 541 CCTGATACACCCAGGGGACCCACCCCTGGCAAGAGCTCCCTCCAGAGACT 600
 Db 716 CCTGATACACCCAGGGGACCCACCCCTGGCAAGAGCTCCCTCCAGAGACT 775
 QY 601 AACAGGGAGTGGCCCTGTCAGCTGGTATGTGTCGGAGGACCGGCTCCCT 660
 Db 776 AACAGGGAGTGGCCCTGTCAGCTGGTATGTGTCGGAGGACCGGCTCCCT 835
 QY 661 GATGTTTACCTGCTGTGAGCTGGCCCAAGTATGGTGGTCCCAATGCCAAC 720
 Db 836 GATGTTTACCTGCTGTGAGCTGGCCCAAGTATGGTGGTCCCAATGCCAAC 895
 QY 721 GCCACCTGCTGTGTCGATACCTGCACCTGCTGCCCAAGACACTGTGTGACTGATC 780
 Db 896 GCCACCTGCTGTGTCGATACCTGCACCTGCTGCCCAAGACACTGTGTGACTGATC 955
 QY 781 CAGAGTATGCTCTCCCAAGGAAAGCTACACGAGACTCTCTCACTAAGCTGCTGGG 840
 Db 956 CAGAGTATGCTCTCCCAAGGAAAGCTACACGAGACTCTCTCACTAAGCTGCTGGG 1015
 QY 841 CACACAGTGGGAGATGTAATGTGCATAGAGTGAAGCTGGCCAGATGGTATACCTGC 900
 Db 1016 CACACAGTGGGAGATGTAATGTGCATAGAGTGAAGCTGGCCAGATGGTATACCTGC 1075
 QY 901 TCCCGTCTACATCGGGGGCTGGGGCTGCTGCCCTTTTACCAGGCTGTGTGCTGAG 960
 Db 1076 TCCCGTCTACATCGGGGGCTGGGGCTGCTGCCCTTTTACCAGGCTGTGTGCTGAG 1135
 QY 961 GACCAATACATGCTGCTGGGGGCTTACGTGTGACAGGAGAGGCTACCTGTGA 1020
 Db 1136 GACCAATACATGCTGCTGGGGGCTTACGTGTGACAGGAGAGGCTACCTGTGA 1195
 QY 1021 CAGGGGGCCCCACAGGTGCTGATGAGAGAGGCCCCAGCTACCTCAGCTGCAGAC 1080
 Db 1196 CAGGGGGCCCCACAGGTGCTGATGAGAGAGGCCCCAGCTACCTCAGCTGCAGAC 1255
 QY 1081 CCACAAGCTTTAAGAGAGATGTCCTGTGATATGTGACAGAGCTGTCCCTCCGAT 1140
 Db 1256 CCACAAGCTTTAAGAGAGATGTCCTGTGATATGTGACAGAGCTGTCCCTCCGAT 1315
 QY 1141 ACCTGCTGCAACTCAAGTCTGGGGAGTGGGGCTGCTGTCCTCAATGCCAAGGCTGCTG 1200
 Db 1316 ACCTGCTGCAACTCAAGTCTGGGGAGTGGGGCTGCTGTCCTCAATGCCAAGGCTGCTG 1375
 QY 1201 TECTGGAACACACAGCACTGTGCCCCAGCATACAGTGTGTAGAGGGGAGTGT 1260
 Db 1376 TECTGGAACACACAGCACTGTGCCCCAGGGCTACAGTGTGTAGAGGGGAGTGT 1435
 QY 1261 CAGCGAGAGAGGAGATGCTGTGACTGTGAGAGAGATGCTGCCCGCGGCTTCCTTA 1320
 Db 1436 CAGCGAGAGAGGAGATGCTGTGACTGTGAGAGAGATGCTGCCCGCGGCTTCCTTA 1495
 QY 1321 TCCCAACCCAGAGACATGGGCTGTGACACGACACACAGTGTGCCCGGTGGGCGAAGCTGC 1380
 Db 1496 TCCCAACCCAGAGACATGGGCTGTGACACGACACACAGTGTGCCCGGTGGGCGAAGCTGC 1555
 QY 1381 TCCCGGAGCCAGAGTGGAGTGGGCTGTGACAGTGTGCCCATCTGTGTGCTGCGAG 1440
 Db 1556 TCCCGGAGCCAGAGTGGAGTGGGCTGTGACAGTGTGCCCATCTGTGTGCTGCGAG 1615
 QY 1441 GATGCGACAGCACTGCTGCCGGCTGCTACACCTGTGACAGGTGAGAGGCTGTGCTGCGAG 1500
 Db 1616 GATGCGACAGCACTGCTGCCGGCTGCTACACCTGTGACAGGTGAGAGGCTGTGCTGCGAG 1675
 QY 1501 AAGGAAGTGTCTGTCGCCAGCTGCTGACCTTCTGCGGCGGAGGCTGACGTTGGTGG 1560
 Db 1676 AAGGAAGTGTCTGTCGCCAGCTGCTGACCTTCTGCGGCGGAGGCTGACGTTGGTGG 1735
 QY 1561 AAGGACGTGAGTGTGGGAGAGACACTTCTGCATGATTAACAGACCTGTGCTCCAGAG 1620
 Db 1736 AAGGACGTGAGTGTGGGAGAGACACTTCTGCATGATTAACAGACCTGTGCTCCAGAG 1795
 QY 1621 AACCGACAGGGCTGGGCTGTGCTCTTACGCCACAGGGGCTGTGTTGTGCTGATCGGCC 1680

Db 1796 AACCGACAGGGCTGGGCTGTGCTCTTACCGGACAGGGGCTGTGTTGTGCTGATCGGCC 1855
 QY 1681 CACTGCTGTCTGCTGGCTTCCGCTGCGACAGGAGGATACCAAGTGTGGCAGAGGAG 1740
 Db 1856 CACTGCTGTCTGCTGGCTTCCGCTGCGACAGGAGGATACCAAGTGTGGCAGAGGAG 1915
 QY 1741 GCCCGCGCTGGGACGCCCCCTTTGAGGAGCCAGGCTTTGAGACAGCTGTGTGAGGAGAC 1800
 Db 1916 GCCCGCGCTGGGAGCGCCCCCTTTGAGGAGCCAGGCTTTGAGACAGCTGTGTGAGGAGAC 1975
 QY 1801 GTACTGAAGACTGTGCAAGCCCTGCGGACCCCACTCGGAGAGTGCCTGTGCTCAGGCTTC 1860
 Db 1976 GTACTGAAGACTGTGCAAGCCCTGCGGAGCCCACTCGGAGAGTGCCTGTGCTCAGGCTTC 2035
 QY 1861 CCTAGCACCTCCCTTACCAATATCTCCCTGGAGCCCAATTCGACATCCCATCACAT 1920
 Db 2036 CCTAGCACCTCCCTTACCAATATCTCCCTGGAGCCCAATTCGACATCCCATCACAT 2095
 QY 1921 GGGAGGTGGGGCTCAATCTAAGGCCCTTCCCTGTGAGAGAGGGGTTGAGGCAAAAGCC - 1979
 Db 2096 GGGAGGTGGGGCTCAATCTAAGG - CCTTCCCTGTGAGAGAGGGGTTGAGGCAAAAGCCA 2154
 QY 1980 CATTAACAGCTGCATGCCCTCCGCTTCAAGTGAACCTGTGAGGAGGCTTTTCCCT 2039
 Db 2155 CATTAACAGCTGCATGCCCTCCGCTTCAAGTGAACCTGTGAGGAGGCTTTTCCCT 2214
 QY 2040 ATCCACAGGGGCTGTGCTGCT 2061
 Db 2215 ATCCACAGGGGCTGTGCTGCT 2236

RESULT 8

AAQ14339

ID AAQ14339 standard; DNA; 1779 Bp.

AC AAQ14339;

XX

AC AAQ14339;

XX

DT 17-JAN-1992 (first entry)

XX

XX

DE Human epithelin precursor.

XX

XX

KW ET; anti-sense RNA; growth regulation; inhibition; stimulation; ss.

XX

OS Homo sapiens.

XX

PH key

FT misc-RNA

FT

XX

XX

PN W09115510-A.

XX

PD 17-OCT-1991.

XX

/note="claim 9, page 54"

41..1819

location/Qualifiers

WT: 1991-325168/44.

P-PSDB: AARI4326.

Shoyab M, Plowman GD;

(BRIM) BRISTOL-MYERS SQUIB.

WPI: 1991-325168/44.

P-PSDB: AARI4326.

Shoyab M, Plowman GD;

(BRIM) BRISTOL-MYERS SQUIB.

WPI: 1991-325168/44.

P-PSDB: AARI4326.

Shoyab M, Plowman GD;

(BRIM) BRISTOL-MYERS SQUIB.

WPI: 1991-325168/44.

P-PSDB: AARI4326.

WT: 1991-325168/44.

P-PSDB: AARI4326.

Shoyab M, Plowman GD;

(BRIM) BRISTOL-MYERS SQUIB.

WPI: 1991-325168/44.

P-PSDB: AARI4326.

Shoyab M, Plowman GD;

(BRIM) BRISTOL-MYERS SQUIB.

WPI: 1991-325168/44.

P-PSDB: AARI4326.

Shoyab M, Plowman GD;

(BRIM) BRISTOL-MYERS SQUIB.

WPI: 1991-325168/44.

P-PSDB: AARI4326.

Shoyab M, Plowman GD;

(BRIM) BRISTOL-MYERS SQUIB.

WPI: 1991-325168/44.

ET-1 and ET-2 were isolated from rat kidneys and their amino acid sequences determined. A full length rat ET cDNA (AA014338) was obtained by screening a rat kidney cDNA library in lambda gt10 with PCR generated ET probes. These probes were also used to obtain the mouse ET gene (AA014340) from a mouse T-cell genomic library. ET DNA was also obtained from human sources (AA014339). An anti-sense ribonucleic acid molecule complementary to the indicated fragment in the features is also claimed. ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others. ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bioactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and, in fact, antagonises this ET-1 activity. See also AA014338-40, AA014952-53, AA014328-9 and AA015315-20.

Sequence 1779 BP; 304 A; 578 C; 547 G; 350 T; 0 other;

Query Match	83.88;	Score 1756.6;	DB 12;	Length 1779;
Best Local Similarity	99.28;	Pred. No. 0;		
Matches 1765; Conservative	0;	Mismatches	0;	Gaps 0;

OY	13	ATGTGGACCCGTGTGAGCTGGGTGGCCCTTAACAGCAGGGCTGGTGGCTGGAGCGCGGTGC	72
Db	1	ATGTGGACCCGTGTGAGCTGGGTGGCCCTTAACAGCAGGGCTGGTGGCTGGAGCGCGGTGC	60
OY	73	CCAGATGGTTCAGTCTGTGCGCTGTGTGGCTGTGCTGGTGGACCCCGGAGAGGCGCACTACAGC	132
Db	61	CCAGATGGTTCAGTCTGTGCGCTGTGTGGCTGTGCTGGTGGACCCCGGAGAGGCGCACTACAGC	120
OY	133	TGCTGTCCGTCGCCCTTCTGTGAGCAATATGGCCACAACACTGTAGCAGGCAATCTGGGTGGACCC	192
Db	121	TGCTGTCCGTCGCCCTTCTGTGAGCAATATGGCCACAACACTGTAGCAGGCAATCTGGGTGGACCC	180
OY	193	TGCGAGGTTGATGCCCACTGCTGTGCGGCGCACTCTGTGATCTTTAACCGTTCAGGAGACT	252
Db	181	TGCGAGGTTGATGCCCACTGCTGTGCGGCGCACTCTGTGATCTTTAACCGTTCAGGAGACT	240
OY	253	TTCGAGTTCGTGCGCCCTTCCAGAGAGCGGTGGAGATGGCGGGATATGGCATCACTGCTGCCCA	312
Db	241	TTCGAGTTCGTGCGCCCTTCCAGAGAGCGGTGGAGATGGCGGGATATGGCATCACTGCTGCCCA	300
OY	313	CGGGGCTTCCACTGCACTGCACTGAGAGAGGGGCGATTCCTGTTCCAAAGATCAGGTAACAATCC	372
Db	301	CGGGGCTTCCACTGCACTGCACTGAGAGAGGGGCGATTCCTGTTCCAAAGATCAGGTAACAATCC	360
OY	373	GTCGGTGCATCCAGTGTGCTGATATGATCACTTGGATATGCCGGAATCTTCCACTGCTGT	432
Db	361	GTCGGTGCATCCAGTGTGCTGATATGATCACTTGGATATGCCGGAATCTTCCACTGCTGT	420
OY	433	GTTATGTCGATATGGCTCTGTGGGGGTGTGTGGCCCATGGCCCGAGGCTTCCTGTGTGAAGAC	492
Db	421	GTTATGTCGATATGGCTCTGTGGGGGTGTGTGGCCCATGGCCCGAGGCTTCCTGTGTGAAGAC	480
OY	493	AGGGTGCATCTGTCTGCGCAAGGTGTCCCTTCTGCGACCTGTGTTACACACCCGCTGCATACACA	552
Db	481	AGGGTGCATCTGTCTGCGCAAGGTGTCCCTTCTGCGACCTGTGTTACACACCCGCTGCATACACA	540
OY	553	CCCAAGGACACCCACCCCTGTGGCAAGAGAGCTCCTGCGCAAGAGATTAACAGGGCAGTG	612
Db	541	CCCAAGGACACCCACCCCTGTGGCAAGAGAGCTCCTGCGCAAGAGATTAACAGGGCAGTG	600
OY	613	GCGCTGTCCACTGTGGTCATGTGTGCGGAGAGCAAGCGTCCCGGGTGGCCCTGATGGTTCTTACC	672
Db	601	GCGCTGTCCACTGTGGTCATGTGTGCGGAGAGCAAGCGTCCCGGGTGGCCCTGATGGTTCTTACC	660
OY	673	TGCTGTGACGTGCCCAAGTGGGAATATATGCTGTGCCCAATGTGCCAAGAGCAGCACTGTCTGC	732
Db	661	TGCTGTGACGTGCCCAAGTGGGAATATATGCTGTGCCCAATGTGCCAAGAGCAGCACTGTCTGC	720
OY	733	TTCGATCACTGTCACTGCTGTGCCCCCAAGACACTGTGTGTGACTGTATCCAGAGTAAGTGC	792
Db	721	TTCGATCACTGTCACTGCTGTGCCCCCAAGACACTGTGTGTGACTGTATCCAGAGTAAGTGC	780

QY	793	CTCTCCAGGAGAACGCTTACCAGGAGACCTTCCTACCTAACCTGCGCTGCCACACACTGGGC	852
Db	791	CTCTCCAGGAGAAACGCTACCAGGAGCTCTCTACTAACTCTCCTGCCACACTGGGG	840
QY	853	GATGTGAATATGTGACATGAGAGTGAAGTGGCCAGATGGCTATACCTGGCTGCCGTATAG	912
Db	841	GATGTGAATATGTGACATGAGAGTGAAGTGGCCAGATGGCTATACCTGGCTGCCGTATAG	900
QY	913	TGCGGGGCTTGGGGCTCTGCTCCCTTTTACCAGGCTGTGTGCTGTGAGGACCATATAC	972
Db	901	TGCGGGGCTTGGGGCTCTGCTCCCTTTTACCAGGCTGTGTGCTGTGAGGACCATATAC	960
QY	973	TGCTGTCCCGGGGGTTTACGTGTGACAGCCAAAGGGATACGTGTGAACAGGGGGCCAC	1032
Db	961	TGCTGTCCCGGGGGTTTACGTGTGACAGCCAAAGGGATACGTGTGAACAGGGGGCCAC	1020
QY	1033	CAGGTGCCCTTGATGAGAGAGGCCCCAGCTACACTCAGCTCCACAGACCCAAAGCCTTG	1092
Db	1021	CAGGTGCCCTTGATGAGAGAGGCCCCAGCTACACTCAGCTCCACAGACCCAAAGCCTTG	1080
QY	1093	AAGAGAGATGTCCCTGTGATTAATGTACAGCTGTCCCTCCTCCGATACCTGCTGCCAA	1152
Db	1081	AAGAGAGATGTCCCTGTGATTAATGTACAGCTGTCCCTCCTCCGATACCTGCTGCCAA	1140
QY	1153	CTCACGCTGGGGGAGTGGGGCTGTGTGCCAATCCAGAGAGGTGTGTCGTCGCGGACAC	1212
Db	1141	CTCACGCTGGGGGAGTGGGGCTGTGTGCCAATCCAGAGAGGTGTGTCGCTCGGACAC	1200
QY	1213	CAGCACTGCTGCCCCCAGACATACAGCTGTGTAGCTGAGAGGGCAGTGTACGAGAGAGC	1272
Db	1201	CAGCACTGCTGCCCCCAGAGGCTACAGCTGTGTAGCTGTGAGAGGGCAGTGTACGAGAGAGC	1260
QY	1273	GAGATCTGTGCTGGACTGTGAGAGAGATGCTGCCCCGCGGTTCTTATCCACCCAGA	1332
Db	1261	GAGATCTGTGCTGGACTGTGAGAGAGATGCTGCCCCGCGGCTTCTTATCCACCCAGA	1320
QY	1333	GACATCGGCTGTGACAGACACACAGCTGCGGTGGGGGGAACGTCGCCCCGAGCCAG	1392
Db	1321	GACATCGGCTGTGACAGACACACAGCTGCGGTGGGGGGAACCTGTGCCGAGCCTG	1380
QY	1393	GGTGGGAGCTGGGCTCTGCTGCCAATGTCGCCATGCTGTGTGCTGCGAGGATGCGCCAGC	1452
Db	1381	GGTGGGAGCTGGGCTCTGCTGCCAGATTGGCCCCATGCTGTGTGCTGCGAGGATGCGCCAGC	1440
QY	1453	TGCTGTCCCGGCTGGCTACACCTGCAAGCTGAAGGCTGCATCTCGGAGAGAGAACTGTC	1512
Db	1441	TGCTGTCCCGGCTGGCTACACCTGCAAGCTGAAGGCTGCATCTCGGAGAGAACTGTC	1500
QY	1513	TCTGCCAGCCTGTGCACCTCTCTGACCCTGAGCCCTCACAGTGGGTGTGAAGACGTGGAG	1572
Db	1501	TCTGCCAGCCTGTGCACCTCTCTGACCCTGAGCCCTCACAGTGGGTGTGAAGACGTGGAG	1560
QY	1573	TGTGGGGAAGACACTTCTGCAATGATTAACAGACCTGCTGCCGAGACAAACCCAGAGGC	1632
Db	1561	TGTGGGGAAGACACTTCTGCAATGATTAACAGACCTGCTGCCGAGACAAACCCAGAGGC	1620
QY	1633	TGGGCTGCTCTCTCCCTACGCCCAAGGCGTGTGTGTGTGATTCGGCGCATCTGCTGCT	1692
Db	1621	TGGGCTGCTCTCTCCCTACGCCCAAGGCGTGTGTGTGTGATTCGGCGCATCTGCTGCT	1680
QY	1693	GCTGGCTTCGCTGCGAGACAGAGGGGTAACTGTTTTCGAGAGGAGAGGCCCGCGCGTG	1752
Db	1681	GCTGGCTTCGCTGCGAGACAGAGGGGTAACTGTTTTCGAGAGGAGAGGCCCGCGCGTG	1740
QY	1753	GACGCCCTTTGAGGAGACCCAGGCTTGAGACACTGCTG	1791
Db	1741	GACGCCCTTTGAGGAGACCCAGGCTTGAGACACTGCTG	1779

Db 371 G---ATAAACCCCTGGGTCGTCTCCAGTGTCTGGAGCCAGTTGAAATGTCCTGACTCT 427
 QY 421 TCACAGCTGCTGTATGATGGATGGCTGCTGAGGGGTGCTGGCCCATGCCCCAGGCTTCC 480
 Db 428 GGCACCTCTGCTGATTTATGTTGATGTTGCTGTTGGGATGTTGTCCTATGCCAGGCTCT 487
 QY 481 TGTCTGGAAGACAGGGTGCACCTGCTGTCGCGACGGTGGCTTCTGCGACCTGGTTACACC 540
 Db 488 TGTCTGGAAGACAGGTCATGCTGTCCTCCATGGGGCTCTCTGTAAGCTGTTGCACACA 547
 QY 541 CGCTGATCACACACCCAGCGGACCCACCCCTGGCAAGAACCTCCCTGCGCCAGAGACT 600
 Db 548 CGATGCTTACACCCAGCGGACCCACACCCCTGTAAGAACTTCTCTGCAACAAAAGAG 607
 QY 601 AACAGGAGTGGCTTGTCCAGCTGGTTCATGTCGCGAGCAGCGGTCGGGTGCTTCC 660
 Db 608 AACAGGAGAGTGTCTTTCCTTTTCTGTCGTGCTGCTGATGCTTAAGACCCAGTGTCC 667
 QY 661 GATGCTTACCTGCTGAGAGTGGCGACATGGGAAATATGGCTGCTGCCAATGCCAAC 720
 Db 668 GATGATTTCTACCTGCTGAGCTGACCTACCTGGAAGTATGGCTGCTGCTCAATGCCAAT 727
 QY 721 GGCACCTGCTGCTGCTGACCTGACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 Db 728 GGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 787
 QY 781 CAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 Db 788 CAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 844
 QY 841 CACACAGTGGCGATGTGAATATGACATGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTG 900
 Db 845 TACCCAGTGAAGAGAGTGAAGTGCACATGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTG 904
 QY 901 TGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 Db 905 TGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 964
 QY 961 GACACATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
 Db 965 GATCATTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1024
 QY 1021 CAGGAGCCCAACAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
 Db 1025 ATGGGTATCTCTCAAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1084
 QY 1081 CCACAGGCTTGAAGAGATGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 Db 1085 CCACAGATCTTGAAGAGATGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1144
 QY 1141 ACCTGCTGCTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
 Db 1145 ACCTGCTGCTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1204
 QY 1201 TGTCTGGAACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
 Db 1205 TGTCTGGAACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1264
 QY 1261 CAGGAGAGAGAGAGATGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 Db 1265 CAGAGGAGAGAGAGATGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1324
 QY 1321 TCCACACCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
 Db 1325 TCCACACCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1384
 QY 1381 TCCACACCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
 Db 1385 TCCACACCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1444
 QY 1441 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
 Db 1445 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1504

QY 1501 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 Db 1505 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 QY 1561 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
 Db 1561 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1618
 QY 1621 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
 Db 1619 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1678
 QY 1681 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
 Db 1679 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1738
 QY 1741 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
 Db 1739 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1798
 QY 1801 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1853
 Db 1799 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1858
 QY 1854 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1912
 Db 1859 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1918
 QY 1913 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1971
 Db 1919 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1978
 QY 1972 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2031
 Db 1979 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2038
 QY 2032 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2069
 Db 2039 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2076
 RESULT 11
 AAVB2824
 ID AAVB2824 standard; cDNA; 2137 BP.
 XX
 AC AAVB2824;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Mouse GP88 autocrine growth factor cDNA.
 XX
 KW GP88; granulins; epithelins; mouse; growth factor; autocrine; tumour;
 KW cancer; viral infection; antagonist; therapy; diagnosis; ss.
 OS Mus sp.
 XX
 FH
 Key Location/Qualifiers
 CDS 23..1792
 FT
 FT /transl_except= (pos:44..45, aa:ile)
 FT /transl_except= (pos:182..184, aa:asp)
 FT /transl_except= (pos:1151..1153, aa:cys)
 FT /transl_except= (pos:1340..1342, aa:leu)
 PN W09852607-A1.
 XX
 PD 26-NOV-1998.
 XX
 PF 22-MAY-1998; 98MO-US10555.
 XX
 PR 16-DEC-1997; 97US-0991862.
 PR 23-MAY-1997; 97US-0863079.

xx (SERR) SERRERO G.

xx Serrero G.

xx WPI: 1999-045276/04.

xx P-PSDB: AAM85474.

xx Composition containing antagonist of growth factor GP88 - useful for
xx treating cancer and viral diseases and also for diagnosing disease
xx from altered GP88 expression

xx Example 5; Fig 8A-D; 86pp; English.

xx This murine cDNA sequence includes a coding region for GP88 (see
xx AAM85474), an 88 kDa glycoprotein autocrine growth factor and
xx epifillin/granulin precursor that is expressed in a tightly
xx regulated manner in normal cells, is overexpressed and upregulated
xx in highly tumorigenic cells derived from normal cells, and which
xx acts as a stringently required growth stimulator for the
xx tumorigenic cells. Inhibition of GP88 expression or action in the
xx properties of the overproducing cells. Murine GP88 cDNA was
xx isolated from the highly tumorigenic PC cell line cDNA library
xx using a probe obtained by PCR using primers based on isolated GP88
xx peptides. Antagonists to GP88 are used to treat diseases
xx associated with increased expression of GP88, particularly cancer
xx but also viral infections. Fragments of GP88 are used to raise
xx and for delivering toxins or other compounds to GP88-expressing
xx cells) and to screen for antibodies. Antisense oligonucleotides
xx can also be used as antagonists. Methods are provided for
xx diagnosing disease, or determining susceptibility to disease,
xx resulting from altered GP88 activity.

xx Sequence 2137 BP; 443 A; 608 C; 583 G; 503 T; 0 other;

xx Query Match 57.5%; Score 1204.8; DB 20; Length 2137;
xx Best Local Similarity 75.8%; Pred. No. 1e-291;

xx Matches 1575; Conservative 0; Mismatches 482; Indels 21; Gaps 6;

QY 1 GCGAGGACACATGTGACACCTGCTGAGCTGGGTGACCTTACAGACGAGGCTGTGCT 60
DB 11 GCGACACAGACATGTGGTCTCTGATGAGCTGGCTCGGCGGACGGCTGTGACCC 70
QY 61 GGAACGCGGTGCGCAGATGTCAGTTCGCTGCTGGCTGCTGCTGCTGCTGCTGCTG 120
DB 71 GGAACAGATGTCAGATGAGGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 130
QY 121 GCGACGTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 131 GCGACGTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 190
QY 181 CTGGGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 191 CTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 250
QY 241 GTCGACGAGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 251 GTCGCTGGGACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 310
QY 301 CACGTCGCGGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 311 CACGTCGCGGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 370
QY 361 GGTAAACACTGCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 371 G---ATAACCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 427
QY 421 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 428 GCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 487

QY 481 TCGCTGAAAGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 488 TCGCTGAAAGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 547
QY 541 CCGTGCATCACACCCAGGCGACCCCTGCGAAGAAAGCTGCTGCTGCTGCTGCTGCTG 600
DB 548 CGATGCTTTCACCCAGGCGACCCCTGCGAAGAAAGCTGCTGCTGCTGCTGCTGCTG 607
QY 601 AACAGGCGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 608 AACAGGCGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 667
QY 661 GATGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 668 GATGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 727
QY 721 GCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 728 GCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 787
QY 781 CAGAGTAAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 788 CAGAGTAAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 844
QY 841 CACACAGTGGCGCATGTGAATGTGACATGAGGTGCTGCTGCTGCTGCTGCTGCTG 900
DB 845 TACCCAGTGAAGGAGTGAATGTGACATGAGGTGCTGCTGCTGCTGCTGCTGCTG 904
QY 901 TCGCGTACAGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 905 TCGCGTACAGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 964
QY 961 GACACATACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
DB 965 GATCATTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1024
QY 1021 CAGGCGCGCCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
DB 1025 ATGGTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1084
QY 1081 CCAACAGCTTGAAGAGATGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
DB 1085 CCAACAGCTTGAAGAGATGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1144
QY 1141 ACCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
DB 1145 ACCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1204
QY 1201 TCGTGGACACACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
DB 1205 TCGTGGACACACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1264
QY 1261 CAGCGAGAGGAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
DB 1265 CAGCGAGAGGAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1324
QY 1321 TCCACCCCGAGACATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
DB 1325 TCCCAATTTGAGANATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1384
QY 1381 TGCCGAGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
DB 1385 TGCCGAGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1444
QY 1441 GATGCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
DB 1445 GATGCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1504
QY 1501 AAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
DB 1505 AAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
QY 1561 AAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620


```

Db 121 TECTTAACCCCTTCTGACACATGCGCTAGAAATPACAGCGCATATCTAATGCTCC 180
Qy 193 TCCAGGTTGATGATCCACTGCTGCGGCGCACCTCGCATCTTTACCTGTCAGAGACT 252
Db 181 TCCAGACCCATGAGGACAGCTGCTGCTGCTATCTTCTCTCTCTCTCTCTCTCTCTCT 240
Qy 253 TCCAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 312
Db 241 TCCAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Qy 313 CGGGCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 372
Db 301 CAGGCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 357
Qy 373 GTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
Db 358 TTTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 417
Qy 433 GTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 492
Db 418 ATTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 477
Qy 493 AGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 552
Db 478 AGAGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 537
Qy 553 CCCAGGCGACCCACCCCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 612
Db 538 CCCAGGCGACCCACCCCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 597
Qy 613 GCTTGTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 672
Db 598 TCTTGTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 657
Qy 673 TGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
Db 658 TGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 717
Qy 733 TCCGATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792
Db 718 TCCGACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 777
Qy 793 CTCTCCAAAGAGACGCTACACAGGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 852
Db 778 CTATCCA--AGAACTACACACAGGATCTCTGACCAACCTGCTGATACCAAGTGAAG 834
Qy 853 GATGGAATGTGATGAGATGAGCTGAGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCT 912
Db 835 GAGGTGAAGTGCATGAGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 894
Qy 913 TCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 972
Db 895 ACTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 954
Qy 973 TECTGTCCCGGCGGCTTACGTGTGACACGACGAGAGGATCTGCTGCTGCTGCTGCTGCT 1032
Db 955 TECTGTCCCGGCGGCTTACGTGTGACACGAGAGAACTGCGCAATGAGGTATCTCTC 1014
Qy 1033 CAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1092
Db 1015 CAAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1074
Qy 1093 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1152
Db 1075 AAGATGATACACCTTGTGATACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1134
Qy 1153 CTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1212
Db 1135 CTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1194
Qy 1213 CAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272

```

```

Db 1195 CAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1254
Qy 1273 GAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1332
Db 1255 ACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1314
Qy 1333 GACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1392
Db 1315 GATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1374
Qy 1393 GGTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1452
Db 1375 AAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1434
Qy 1453 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1512
Db 1435 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1494
Qy 1513 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1572
Db 1495 TTTATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1548
Qy 1573 TGTGGGGAAGGACACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1632
Db 1549 TGTGGAAGGAGGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1608
Qy 1633 TGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1692
Db 1609 TGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1668
Qy 1693 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1752
Db 1669 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1728
Qy 1753 GACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1791
Db 1729 GACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1767

RESULT 14
AAA69779/c
ID AAA69779 standard; cDNA; 561 BP.
XX
XX AAA69779;
XX
XX 07-NOV-2000 (first entry)
XX
DE Human ovarian carcinoma antigen polynucleotide SEQ ID NO:89.
XX
XX Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
XX tumour antigen; identification; cytostatic; gene therapy; vaccine; ss.
XX
XX Homo sapiens.
XX
XX WO200036107-A2.
XX
XX 22-JUN-2000.
XX
XX 17-DEC-1999; 99WO-US30270.
XX
XX 17-DEC-1998; 98US-0215681.
XX 17-DEC-1998; 98US-0216003.
XX 23-JUN-1999; 99US-0338933.
XX 24-SEP-1999; 99US-0404879.
XX
XX (CORI-) CORIXA CORP.
XX
XX Mitcham Jr, King GE, Algate PA, Frudakis TN;
XX
XX WPI; 2000-431589/37.
XX
XX Immunogenic portion of an ovarian carcinoma protein and the nucleic
XX acid encoding it, useful for the diagnosis, prevention and treatment of

```


Search completed: February 21, 2003, 13:05:06
Job time : 486 secs

A

A

A

Source 1. .2095
/organism="unknown"
BASE COUNT 364 a 682 c 624 g 425 t
ORIGIN

Query Match 100.0%; Score 2095; DB 6; Length 2095;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2095; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGCAGGACGACATGTGACCCCTGTGAGCTGGTGGCTTAAACAGCAGGGCTGTGGCT 60
1 CGCAGGACGACATGTGACCCCTGTGAGCTGGTGGCTTAAACAGCAGGGCTGTGGCT 60
1 CGCAGGACGACATGTGACCCCTGTGAGCTGGTGGCTTAAACAGCAGGGCTGTGGCT 60
61 GGAACGGGTGGCCAGATGTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 120
61 GGAACGGGTGGCCAGATGTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 120
121 GCCACTACAGTGTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 180
121 GCCACTACAGTGTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 180
181 CTGGGTGCCCCCTGCGAGGTTGATGCTCCACTGCTGCGGCGCACTCCGATCTTTACC 240
181 CTGGGTGCCCCCTGCGAGGTTGATGCTCCACTGCTGCGGCGCACTCCGATCTTTACC 240
181 CTGGGTGCCCCCTGCGAGGTTGATGCTCCACTGCTGCGGCGCACTCCGATCTTTACC 240
241 GTCTAGGAGACTTCCAGTTGCTGCCCTTCCAGAGCCGCTGGCATGCGGGGATGGCAT 300
241 GTCTAGGAGACTTCCAGTTGCTGCCCTTCCAGAGCCGCTGGCATGCGGGGATGGCAT 300
301 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
301 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
361 GGTAAACAATCCGCTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
361 GGTAAACAATCCGCTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
421 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
421 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
481 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
481 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
481 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
541 CGCTCATACACACCCAGGAGCCACCCCTGCGCAAGAAAGACTCCCTGCGCAGAGACT 600
541 CGCTCATACACACCCAGGAGCCACCCCTGCGCAAGAAAGACTCCCTGCGCAGAGACT 600
601 AACAGGAGAGTGGCTTGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
601 AACAGGAGAGTGGCTTGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
661 GATGTTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
661 GATGTTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
721 GGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
721 GGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
721 GGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
781 CAGAGTAAAGTGGCTTCCAAAGAGAAAGCTACACGAGACTCTCTCACTAAGAGTGGCTG 840
781 CAGAGTAAAGTGGCTTCCAAAGAGAAAGCTACACGAGACTCTCTCACTAAGAGTGGCTG 840
841 CACACAGTGGGAGATGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
841 CACACAGTGGGAGATGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
841 CACACAGTGGGAGATGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
901 TCCCTTACAGTGGGAGATGTAATGATGATGATGATGATGATGATGATGATGATGATGATG 960
901 TCCCTTACAGTGGGAGATGTAATGATGATGATGATGATGATGATGATGATGATGATGATG 960

961 GACCACATACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
961 GACCACATACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
1021 CAGGGGGCCACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
1021 CAGGGGGCCACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
1081 CCACAGGCTTGAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
1081 CCACAGGCTTGAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
1141 ACCTGCTGCAATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
1141 ACCTGCTGCAATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
1201 TGTCTGGACACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
1201 TGTCTGGACACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
1261 CAGCGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
1261 CAGCGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
1321 TCCACCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
1321 TCCACCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
1381 TCCCGAGCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
1381 TCCCGAGCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
1441 GATGCGCAGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
1441 GATGCGCAGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
1501 AAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
1501 AAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
1561 AAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
1561 AAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
1621 AACGACAGGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
1621 AACGACAGGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
1681 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
1681 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
1741 GCGCGGCTGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
1741 GCGCGGCTGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
1801 GTACTGAAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
1801 GTACTGAAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
1861 CCTAGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
1861 CCTAGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
1921 GGGAGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
1921 GGGAGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
1981 ATTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
1981 ATTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
2041 TCCACAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2095

```

Db 2041 TCCACAGCGGTGTTGTGGTGGTGTTCATTAAGATTGTCACTTCTT 2095
|||||
RESULT 2
HOMGRANUL. 2095 bp mRNA linear PRI 31-DEC-1994
LOCUS HOMGRANUL. 2095 bp mRNA linear PRI 31-DEC-1994
DEFINITION H.sapiens granuln mRNA, complete cds.
ACCESSION M75161
VERSION M75161.1 GI:183612
KEYWORDS granuln.
SOURCE Homo sapiens (tissue library: Clontech HL1058b) adult bone marrow
mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homilidae; Homo.
REFERENCE 1 (bases 1 to 2095)
AUTHORS Bhandari,V., Palfrey,R.G. and Bateman,A.
TITLE Isolation and sequence of the granuln precursor cDNA from human
bone marrow reveals tandem cysteine-rich granulin domains
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (5), 1715-1719 (1992)
MEDLINE 92179253
PUBMED 1542665
FEATURES
Source
1..2095
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="bone marrow"
/dev_stage="adult"
/tissue_lib="Clontech HL1058b"
1..2095
/gene="granulin"
13..1794
/gene="granulin"
/codon_start=1
/product="granulin"
/protein_id="AAAS8617.1"
/db_xref="GI:183613"
/translacion="MNTLVSNVLTAGLVAGTRCPDGFPCVACCLDPGASYSRCP
LLDKWPTLSRLHSGPCOVDAHSCASGHSCTIFVSGTSCCPPEAVACGDHHCPRG
FHCSADGSRCSFRSGNSNSVGLICDPSDFECPDSTCCVMDGSGCPMPGASCCED
RVHCCPHAFCDLVHTRCITPTGTHPLAKKLPAQNTNNAVALSSVMCPDARSCEPDG
STCELPFGKGGCCPMATCCSDHLHCCPDQVCDLQSKCLSEMTTDLTLPLA
HTVDVCKDMVSCPDYTCCLRLSGANGCCPTQAVCCEDHICCPAGFTCDTQKGT
EACGSHQVPMMEKAPAHLSLPDQALKRSDVCDNVSPPSDTCCPLDISEGACCPIP
EAVCCSDHCCCPQRYTCVAGCCOCGSEIYGLKEMARBSLSHPDIDGDDHTSC
PVGGCCPSOGGSNACCOLPHAVCCEDRHHCCPAGTCNTVARSCEKEVYSNAPATFL
ARSPHYGVKDYECGEGHCHDNQTCRPNRSGMACCPYAQGVCCADRRHCCPAGFRCA
RRTKCLRRKRAPRMADPLRDPALROLL"
13..63
/gene="granulin"
/note="presumed signal peptide"
64..1791
/gene="granulin"
/product="granulin"
/note="presumed mature peptide"
2075..2080
/gene="granulin"
BASE COUNT 364 a 682 c 624 g 425 t
ORIGIN
Query Match 100.0%; Score 2095; DB 9; Length 2095;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2095; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCAGGACACCATGTGACCTGTGAGCTGGTGGCTTAAACAGCAGGCGTGGCT 60
|||||
Db 1 CCCAGGACACCATGTGACCTGTGAGCTGGTGGCTTAAACAGCAGGCGTGGCT 60
QY 61 GGAACGCGGTGCCAGATGATGTCTGCTGCTGGCTGCTGCTGACCCCGAGGA 120
|||||
Db 61 GGAACGCGGTGCCAGATGATGTCTGCTGCTGCTGCTGCTGACCCCGAGGA 120

```

```

QY 121 GCCAGCTACAGCTGTCGCCGTCCTCCCTTCTGACAAATGGCCCAACACTGACGAGCAT 180
|||||
Db 121 GCCAGCTACAGCTGTCGCCGTCCTCCCTTCTGACAAATGGCCCAACACTGACGAGCAT 180
QY 181 CTGGGTGGCCCTTCCAGAGTGTATGCCACTGCTTGGCGGACATCTGCACTTTACC 240
|||||
Db 181 CTGGGTGGCCCTTCCAGAGTGTATGCCACTGCTTGGCGGACATCTGCACTTTACC 240
QY 241 GTCTCAGGACCTCCAGTTGCTGCCCTTCCAGAGCCGTGGCATAGCGGGGATGGCCAT 300
|||||
Db 241 GTCTCAGGACCTCCAGTTGCTGCCCTTCCAGAGCCGTGGCATAGCGGGGATGGCCAT 300
QY 301 CACTGTGCCACAGGGGCTTCCACTGCAGTGCAGAGCGGGGATCTGCTTCCAAATCA 360
|||||
Db 301 CACTGTGCCACAGGGGCTTCCACTGCAGTGCAGAGCGGGGATCTGCTTCCAAATCA 360
QY 361 GGTAAACATCTCCGTGGGTGCTATCCAGTGGCTGATATGATGATTTGAAATGCCGACTTC 420
|||||
Db 361 GGTAAACATCTCCGTGGGTGCTATCCAGTGGCTGATATGATGATTTGAAATGCCGACTTC 420
QY 421 TCCAGCTGCTGTATTATGTCATGATGCTCTGGGGGTGCTGCCCATGCCCCAGGGCTTC 480
|||||
Db 421 TCCAGCTGCTGTATTATGTCATGATGCTCTGGGGGTGCTGCCCATGCCCCAGGGCTTC 480
QY 481 TGCTGTGAAGACAGGGTGCACTGCTGTCGACAGGTGCTTTCGCACTGTTCAACC 540
|||||
Db 481 TGCTGTGAAGACAGGGTGCACTGCTGTCGACAGGTGCTTTCGCACTGTTCAACC 540
QY 541 CGCTGATCAACACCCAGGGGACACCCCTTGGCAAGAAGTCCCTGCCAGAGACT 600
|||||
Db 541 CGCTGATCAACACCCAGGGGACACCCCTTGGCAAGAAGTCCCTGCCAGAGACT 600
QY 601 AACAGGACAGTGGCTTGTGTCAGCTGCTGATGTCGTCGAGCAGAGGTCGGGTGCTTC 660
|||||
Db 601 AACAGGACAGTGGCTTGTGTCAGCTGCTGATGTCGTCGAGCAGAGGTCGGGTGCTTC 660
QY 661 GATGTTCTACCTGCTGTGAGTGCACAGTGGGAATGGCTGTCGCCAATGCCAAC 720
|||||
Db 661 GATGTTCTACCTGCTGTGAGTGCACAGTGGGAATGGCTGTCGCCAATGCCAAC 720
QY 721 GCCACTGCTGCTCCGATCACTGCTGACTGTGCCCCAGACACTGTGTACTGATC 780
|||||
Db 721 GCCACTGCTGCTCCGATCACTGCTGACTGTGCCCCAGACACTGTGTACTGATC 780
QY 781 CAGAGTAAGGCTCTTCGAAGAGAAAGCTTACACAGGACTCTCTACTAAGCTGCTGG 840
|||||
Db 781 CAGAGTAAGGCTCTTCGAAGAGAAAGCTTACACAGGACTCTCTACTAAGCTGCTGG 840
QY 841 CACACAGTGGCGATGTGAATGTGACATGAGAGTGAAGTGCACAGATGGCTATACCTGC 900
|||||
Db 841 CACACAGTGGCGATGTGAATGTGACATGAGAGTGAAGTGCACAGATGGCTATACCTGC 900
QY 901 TGCGGTCTACAGTCCGGGGGCTGCTGCTGCTTTTACCAGGCTGTGTCTGTGAG 960
|||||
Db 901 TGCGGTCTACAGTCCGGGGGCTGCTGCTGCTTTTACCAGGCTGTGTCTGTGAG 960
QY 961 GACCAATACACTGCTGTCGCCGGGGTTTACGTGTGACACGAGAGGTTACTGTGAA 1020
|||||
Db 961 GACCAATACACTGCTGTCGCCGGGGTTTACGTGTGACACGAGAGGTTACTGTGAA 1020
QY 1021 CAGGGGCCCCACAGGTGCTGCTGATGAGAGAGGCCCCACCTCAGCTGACGCTCCAGAC 1080
|||||
Db 1021 CAGGGGCCCCACAGGTGCTGCTGATGAGAGAGGCCCCACCTCAGCTGACGCTCCAGAC 1080
QY 1081 CCACAGCTTGAAGAGATGTCCTGTGATAATGTACGACGTGTCTCTCCGAT 1140
|||||
Db 1081 CCACAGCTTGAAGAGATGTCCTGTGATAATGTACGACGTGTCTCTCCGAT 1140
QY 1141 ACCTGTGCCAATCAAGTGTGGGAGTGGGCTGCTGTCATATCCAGAGGCTGTCTGC 1200
|||||
Db 1141 ACCTGTGCCAATCAAGTGTGGGAGTGGGCTGCTGTCATATCCAGAGGCTGTCTGC 1200
QY 1201 TGCTGGACACACAGCAGTGTGCTGCCCCACAGCATACAGTGTGTAGCTGAGGGGCAGTGT 1260

```


Db	1201	TGCTCGGACCA	CAGCACTGCTG	CCCGCCAGGATAC	AGTGTGTAGTGA	GGGGAGTGT	1260
Qy	1261	CAGGAGAAAC	CGAGATCTGTG	CTGTGAC	TGGAGAAGAT	CCCTGCCCGCGGGTCTT	1320
Db	1261	CAGGAGAAAC	CGAGATCTGTG	CTGTGAC	TGGAGAAGAT	CCCTGCCCGCGGGTCTT	1320
Qy	1321	TCCCACCC	CCAGACATCGG	CTGTGAC	CAGACACAC	CACTCCCGGTGGGGAACTGC	1380
Db	1321	TCCCACCC	CCAGACATCGG	CTGTGAC	CAGACACAC	CACTCCCGGTGGGGAACTGC	1380
Qy	1381	TGCGGAGCC	AGAGGTGGG	AGCTGGG	CGCTGCTGCC	AGTTGCCCATGCTGTGTGTCGAG	1440
Db	1381	TGCGGAGCC	AGAGGTGGG	AGCTGGG	CGCTGCTGCC	AGTTGCCCATGCTGTGTGTCGAG	1440
Qy	1441	GATCGCAG	CACACTGTCC	CGGCGGTAC	ACCTGCACAC	GTGAAGGCGTCGATCCCTGGAG	1500
Db	1441	GATCGCAG	CACACTGTCC	CGGCGGTAC	ACCTGCACAC	GTGAAGGCGTCGATCCCTGGAG	1500
Qy	1501	AAGGAAGT	GTCTCTGTGCC	CACGCTGCC	ACCTTCTGTGG	CCCGTAAGCCCTCAACGTGGGTGTG	1560
Db	1501	AAGGAAGT	GTCTCTGTGCC	CACGCTGCC	ACCTTCTGTGG	CCCGTAAGCCCTCAACGTGGGTGTG	1560
Qy	1561	AAGAGAGT	GTGAGTGGGG	AAGAGACACTT	CTGCATATTA	ACAGACACTCTGCCAGAC	1620
Db	1561	AAGAGAGT	GTGAGTGGGG	AAGAGACACTT	CTGCATATTA	ACAGACACTCTGCCAGAC	1620
Qy	1621	AACCGAC	AGAGGCTGGG	CGCTGCTCC	CTACGCC	CAGGGCGTGTGTGCTGATCGAGCG	1680
Db	1621	AACCGAC	AGAGGCTGGG	CGCTGCTCC	CTACGCC	CAGGGCGTGTGTGCTGATCGAGCG	1680
Qy	1681	CACGTGTC	CTGTGCTGCTCC	CTCGCTCGCAC	AGAGGGGTAC	AAAGTTTGCCACAGGAG	1740
Db	1681	CACGTGTC	CTGTGCTGCTCC	CTCGCTCGCAC	AGAGGGGTAC	AAAGTTTGCCACAGGAG	1740
Qy	1741	GGCCGCGC	CTGGGACGCC	CCCTTTGAG	GGGACCCAG	CCCTTGAGACAGCTGTGAGGGACA	1800
Db	1741	GGCCGCGC	CTGGGACGCC	CCCTTTGAG	GGGACCCAG	CCCTTGAGACAGCTGTGAGGGACA	1800
Qy	1801	GTACTGA	AGACTGTG	AGGCTTC	GGAGCCCACT	TGGAGGGTGGCCCTGCTAGAGCTTC	1860
Db	1801	GTACTGA	AGACTGTG	AGGCTTC	GGAGCCCACT	TGGAGGGTGGCCCTGCTAGAGCTTC	1860
Qy	1861	CCTAGCACT	CCCCCTTA	ACCAAAATTC	CTCCCTGG	AGCCCACTTGAGCTCCCATACAT	1920
Db	1861	CCTAGCACT	CCCCCTTA	ACCAAAATTC	CTCCCTGG	AGCCCACTTGAGCTCCCATACAT	1920
Qy	1921	GGGAGTGG	GGGCTCAAT	CTAAGG	CCCTTCCCTGT	CAAGAGGGGTTGAGGCAAAAGGCC	1980
Db	1921	GGGAGTGG	GGGCTCAAT	CTAAGG	CCCTTCCCTGT	CAAGAGGGGTTGAGGCAAAAGGCC	1980
Qy	1981	ATTACAAC	CTGCATCC	CCCTCCG	GTTCAGTGA	ACCCTGTGGCCAGAGTCTTTTCCCTA	2040
Db	1981	ATTACAAC	CTGCATCC	CCCTCCG	GTTCAGTGA	ACCCTGTGGCCAGAGTCTTTTCCCTA	2040
Qy	2041	TCCACAGG	GGTGTGTGTG	GGGTGTG	CTTCAAT	AAAGTTTTCACATTTCTT	2095
Db	2041	TCCACAGG	GGTGTGTGTG	GGGTGTG	CTTCAAT	AAAGTTTTCACATTTCTT	2095

[illegible]

AUTHORS	Strausberg, R.
TITLE	Direct Submision
JOURNAL	Submitted (10-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: Villalona@bcm.tmc.edu . Villalona, D.R., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAX Plate: 12 Row: a Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10435243 Location/Qualifiers

```

/organism="Homo sapiens"
/db_xref="locusID:2896"
/db_xref="taxon:9606"
/clone="MGC:9342 IMAGE:3457813"
/tissue_type="Cervix, carcinoma"
/clone_1ib="NH_MGC_12"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
32..1813
/codon_start=1

```

```

/protein_id="AAH10577.1"
/db_xref="GI:147114851"
/translation="MTVLISWVALTAGLVAGTRCPDGFQFVACILIDPAGSYSCSRP
ILDKPTTLISRLHGGPCVDVAHCSAGSGICFTYVSGTSCDPEPAVACGGHHCCPGP
FHKSADRGSCFORSGNNSVGAIOCPDPSDFECPDSTCCVAYDSDGSGCCPMQASCCED
RVHCCPGARGCYDLVHTRCITPTGTGHPILAKPLIPORTNRAVALSSVSCPPARSCPCDG
STCCGLPBGATGCGCPMPNATCCSDHLKCCQDDYVCDILQSKCLSKENATDILTLKLP
HIVGDKVCDMEVSCPDYTCRQLQSGMGCCPTQAVCCSDHILHCCPAGTCDPQKCT
CEQGGPDMMERKAPAHILSLDPOALTRDVCVGNVSSCPSSDTCCLQTSSEMCCGPI
EAGCCSDHHCCKPOGATYCVAGLQDQORSESLVAGLEKNKPARASLSHRDITGCDQHTL
PVQGTCCPSLGSIMACCOLPRAVNCCEBRQHCPCAGTCCNARKSCKEEVSAPATFL
ARSPHYGVKDYVECGEGHCFCHDNOTCCENQGNACCPYRGVCCADRRHCCPAGFRCA
ARQTKLIRRAPMPWDELPLRDPLROLL"

```

Query Match	96.1%	Score 2014:	DB 9;	Length 2132;
Best Local Similarity	99.28;	Pred. No. 0;		
Matches 2045;	Conservative	0;	Mismatches 15;	Indels 2;
				Gaps 2;
QY	1	CGCAGCGACACCATGTGACCTTGTAAGCTGGGTGACCTTAAACAGCAGGAGCTGTGGCT	60	
Db	20	CGCAGCGACAGACCATGTGTGACCTGTGAGCTGGGTGACCTTAAACAGCAGGAGCTGTGGCT	79	
QY	61	GGAACGGCGGTGCCAGATGTGCAATTTGTGCCCTGTGGCCGTGCCTCGGACCCCGGAGGA	120	
Db	80	GGAACGGCGGTGCCAGATGTGCAATTTGTGCCCTGTGGCCGTGCCTCGGACCCCGGAGGA	139	
QY	121	GCGAGGTACAGCTGCTGCGCGCTCCCTCTGTGAAATAATGCCCAACACTGAGCAGGCAT	180	
Db	140	GCGAGGTACAGCTGCTGCGCGCTCCCTCTGTGAAATAATGCCCAACACTGAGCAGGCAT	199	
QY	181	CTGGGTGGCCCCCTGCAGGTTGATGGCCCACTGCTGTGGCGGCACTTCCTACATCTTACC	240	

Db 200 CTGGGTGGCCCTTCAGATTGATGCCACTGCTTCGCCGCCACTCTGCATCTTTACC 259
 QY 241 GTTCAGAGGACTTCAGATTGCTGCCCTTCCAGAGCCGTGGCATGCGGGGATGCCAT 300
 Db 260 GTCTCAGGAGACTTCAGATTGCTGCCCTTCCAGAGCCGTGGCATGCGGGGATGCCAT 319
 QY 301 CACTGCTGCCACGGGGCTTCAGTGCAGTGCAGAGGGGCATCTGCTTCCAAAGATCA 360
 Db 320 CACTGCTGCCACGGGGCTTCAGTGCAGTGCAGAGGGGCATCTGCTTCCAAAGATCA 379
 QY 361 GGTAAACATCCGTGGGGTCCATCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 420
 Db 380 GGTAAACATCCGTGGGGTCCATCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 439
 QY 421 TCCAGTGTCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 Db 440 TCCAGTGTCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 499
 QY 481 TGCCTGAAGACAGGGTGCATGCTGTCCGACAGGTGCTTCTGCGACCTGTTACACAC 540
 Db 500 TGCCTGAAGACAGGGTGCATGCTGTCCGACAGGTGCTTCTGCGACCTGTTACACAC 559
 QY 541 CGCTGACATACACCCAGGGGACCCACCCTGGCAAGAAAGCTCCCTGCCAGAGGACT 600
 Db 560 CGCTGACATACACCCAGGGGACCCACCCTGGCAAGAAAGCTCCCTGCCAGAGGACT 619
 QY 601 AACAGGACAGTGGCTTGTCCAGTGTCCAGTGTCCAGTGTCCAGTGTCCAGTGTCCAG 660
 Db 620 AACAGGACAGTGGCTTGTCCAGTGTCCAGTGTCCAGTGTCCAGTGTCCAGTGTCCAG 679
 QY 661 GATGCTTCTACCTGCTGTGAGACTGCCAGTGGGAAGTATGGCTGCTGCCAATGCCCCAAC 720
 Db 680 GATGCTTCTACCTGCTGTGAGACTGCCAGTGGGAAGTATGGCTGCTGCCAATGCCCCAAC 739
 QY 721 GCCACTGCTGCTCGATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 Db 740 GCCACTGCTGCTCGATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 799
 QY 781 CAGAGTAACTGCTTCCAGAGAAAGCTACACGAGCTCTCTCACTAACTGCTGCTGCTG 840
 Db 800 CAGAGTAACTGCTTCCAGAGAAAGCTACACGAGCTCTCTCACTAACTGCTGCTGCTG 859
 QY 841 CACACAGTGGGCGATGTGAATGTGACATGAGAGTGCAGTGCAGTGCAGTGCAGTGCAG 900
 Db 860 CACACAGTGGGCGATGTGAATGTGACATGAGAGTGCAGTGCAGTGCAGTGCAGTGCAG 919
 QY 901 TGCCTGTACAGTGGGGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 Db 920 TGCCTGTACAGTGGGGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 979
 QY 961 GACCACATACACTGCTGTCCGCGGGGTTTACGTGTGACAGCGCAGAAAGGTACTGTGTA 1020
 Db 980 GACCACATACACTGCTGTCCGCGGGGTTTACGTGTGACAGCGCAGAAAGGTACTGTGTA 1039
 QY 1021 CAGGGGCCCCCAGAGTGCCTGATGAGAAAGGCCCACTACCTACCTGCTGCTGCTGCTG 1080
 Db 1040 CAGGGGCCCCCAGAGTGCCTGATGAGAAAGGCCCACTACCTACCTGCTGCTGCTGCTG 1099
 QY 1081 CCACAGAGCTTGAAGAGATGTCCCTGTATATGTCAGAGTGTCCCTGCTGCTGCTGCTG 1140
 Db 1100 CCACAGAGCTTGAAGAGATGTCCCTGTATATGTCAGAGTGTCCCTGCTGCTGCTGCTG 1159
 QY 1141 ACCTGTGCCAATCAGTGTGGGAGTGGGCTGCTGTCCATTCACAGAGGCTGTGCTG 1200
 Db 1160 ACCTGTGCCAATCAGTGTGGGAGTGGGCTGCTGTCCATTCACAGAGGCTGTGCTG 1219
 QY 1201 TGCCTGGAACACAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
 Db 1220 TGCCTGGAACACAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1279
 QY 1261 CAGGAGGAAGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 Db 1280 CAGGAGGAAGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1339

QY 1321 TCCACACCCAGAGACATGCGCTGTGTACACAGACACACAGCTGCCGGTGGGCGGAACCTGC 1380
 Db 1340 TCCACACCCAGAGACATGCGCTGTGTACACAGACACACAGCTGCCGGTGGGCGGAACCTGC 1399
 QY 1381 TGCCTGAGCCAGGCTGGGAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
 Db 1400 TGCCTGAGCCAGGCTGGGAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1459
 QY 1441 GATGCGCACACTGCTGCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
 Db 1460 GATGCGCACACTGCTGCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1519
 QY 1501 AAGGAAGTGTCTGCTGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 Db 1520 AAGGAAGTGTCTGCTGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1579
 QY 1561 AAGGAGTGTGAGTGTGGGAGAGGACACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
 Db 1580 AAGGAGTGTGAGTGTGGGAGAGGACACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1639
 QY 1621 AACCGACAGGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
 Db 1640 AACCGACAGGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1699
 QY 1681 CACTG 1740
 Db 1700 CACTG 1759
 QY 1741 GCCCGCGCTGGGAGCCCTTTTGAAGGACACAGCTTGAAGAGCTGCTGTGAGGAGACA 1800
 Db 1760 GCCCGCGCTGGGAGCCCTTTTGAAGGACACAGCTTGAAGAGCTGCTGTGAGGAGACA 1819
 QY 1801 GTACTGAACACTGTGAGGCTGAGGCTGAGGACCCACTGAGGAGGCTGCTGCTGCTGCTGCTG 1860
 Db 1820 GTACTGAACACTGTGAGGCTGAGGCTGAGGACCCACTGAGGAGGCTGCTGCTGCTGCTGCTG 1879
 QY 1861 CCTAGACCTCCCTTACCAAAATTCCTGTGAGACCCCAATTCGACTGCCATCAACAT 1920
 Db 1880 CCTAGACCTCCCTTACCAAAATTCCTGTGAGACCCCAATTCGACTGCCATCAACAT 1939
 QY 1921 GGGAGTGGGCTGCAATTAAGGCTTCCCTGCTGAGAAAGGGGCTGAGGCAAAAAGCC- 1979
 Db 1940 GGGAGTGGGCTGCAATTAAGG-CTTTCCTGTGAGAAAGGGGCTGAGGCAAAAAGCC 1998
 QY 1980 CATTAACACTGCAATCCCTCCCTGCTGAGGAGCCCTGAGGAGGCTTTCCTGCTGCTGCTGCTG 2039
 Db 1999 CATTAACACTGCAATCCCTCCCTGCTGAGGAGCCCTGAGGAGGCTTTCCTGCTGCTGCTGCTG 2058
 QY 2040 ATCCACAGGGGTGTTGTGTGT 2061
 Db 2059 ATCCACAGGGGTGTTGTGTGT 2080
 RESULT 4
 HSEPT1
 LOCUS HSEPT1 2152 bp mRNA linear PRI 26-AUG-1992
 DEFINITION H. sapiens mRNA for epithelin 1 and 2.
 ACCESSION X62320.1
 VERSION X62320.1 GI:31192
 KEYWORDS epithelial cell growth regulator; Epithelin 1; Epithelin 2; soluble protein.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 2152)
 PLOWMAN, G.D., GREEN, J.M., NEUBAUER, M.G., BUCKLEY, S.D.,
 McDONALD, V.L., TODARO, G.J. and SHOYAB, M.
 The epithelin precursor encodes two proteins with opposing
 activities on epithelial cell growth
 JOURNAL J. Biol. Chem. 267 (18), 13073-13078 (1992)
 MEDLINE 92317004

Source

CDS

```

41..1822
A1clone.t110~PCR clones in Bluescript+
/codon_start=1
/product="Epithelin 1 & 2"
/protein_id="CAA44196.1"
/db_xref="GI:31193"
/db_xref="SWISS-PROT:P28799"
/translation="MTLVSVAMHILVGLVAGTRCPDGPQCPVACCLIDPGGASVSGCRRL
LIDKRPPTLSLHSLGCPQVQVHLSASGHSCTFYVSGTSSCCPPPELVACGGDGHCCPG
RHCSADNGSCQKRSNGNSVAIICPPQLEKCPFRNVCVWNGSSCCPMQASCCED
RHCCPHAFEDLVHTNCTIPCTPTTCLPSKCEPFRNVAIVLSSGSMEDMRSCPDG
STCLDPGKAGGCCPMENATCCSDHLCGDDPQYVCLIOSKTSKNAITDLNTRKLPAA
HTVDVACDKMEVSCPDDYTCCTCRISGASMGCCPFQVAVCCEDHITCCPAGFTGMOCKP
CEQGPDPVPMMEKPAALSLPDQQAIRVUPRDVNSCCSSSOTCOLTFSGEMQCTIP
EAVCCSHDHCQCPGGYTCVAGGCGQCGMSITVAGLEKMPARRRSLSHMPIDLDGHTS
PVGTGCPCCSLGSSMACCOLPHANCCEDRHCQCPAUYTVNARSCEKVSQAQPAFL
ARSHVAGVCKVEGCEGFCFHCDNTCCRRDRMGACCPEYGGVCCADRHCCPAGFCA
11 91
ARGCKTLRRAPMMDALNRPDNTROLL"

```

BASE COUNT	394	a	691	c	639	g	428	t
sig_peptide	41	.91						
mat_peptide	92	.1819						
misc_feature	/product="Epithelin 1 & 2"	215	.382					
misc_feature	/note="cysteine motif 1"	392	.394					
misc_feature	/note="pot. glycosylation site"	410	.580					
misc_feature	/note="cysteine motif 2"	656	.826					
misc_feature	/note="Epithelin 2"	746	.748					
misc_feature	/note="pot. glycosylation site"	833	.835					
misc_feature	/note="pot. glycosylation site"	884	.1051					
misc_feature	/note="Epithelin 1"	1130	.1294					
misc_feature	/note="cysteine motif 5"	1142	.1144					
misc_feature	/note="pot. glycosylation site"	1364	.1531					
misc_feature	/note="cysteine motif 6"	1595	.1762					
misc_feature	/note="cysteine motif 7"	1628	.1630					
misc_feature	/note="pot. glycosylation site"							

Query Match	Score 2014;	DB 9;	Length 2152;
Best Local Similarity	96.1%;		
Matches 2045; Conservative	99.2%;		
	Pred. No. 0;		
	0; Mismatches	15; Indels	2

OY	1	CGCAGGAGACCAATGTGTGACCCTGGTGGACTGGGTGGCCCTTAACAACAGAGGGCTGTGGCT	60
Db	29	CGCAGGAGACCAATGTGTGACCCTGGTGGACTGTGGGTGGCCCTTAACAAGAGGGCTGTGGCT	88
OY	61	GGAACGGGGGCCCAATGCTCATTTCTGCCTGTGGCTCTGCTCTGAGACCCGGAGGA	120
Db	89	GGAACGGGGGCCCAATGCTCATTTCTGCCTGTGGCTCTGCTCTGAGACCCGGAGGA	148
OY	121	GCCAGCTAACGCTGTCTGCCCTCCCTCTTGAGCAAATGTGGCCCAACACACTGAGACAGGCAT	180

Db	149	GCACGCTACAGGCTGCTGCCGTCCTCTGTGGACAAATGGCCCAACACATGAGCAGCAT	208
Qy	181	CTGGGGTGGCCCTGCGCAGGTTGATGCCACATGCTGTGCGGGCACATCCGATCTTAAAC	240
Db	209	CTGGGGTGGCCCTTGCACAGTTGATGGCCACATGCTGTGCGGGCACATCTTAAAC	268
Qy	241	GTCTCAGGACTTCCAGTTGCTGGCCCTTCCAGAGCCGTGGCATGCGGGGATGGCAT	300
Db	269	GTCTCAGGACTTCCAGTTGCTGGCCCTTCCAGAGCCGTGGCATGCGGGGATGGCAT	328
Qy	301	CACCTGTGCCACAGGGGCTTCCACTGTGACGTGAGCGAGGGGAGATCCATGCTTCAAGATCA	360
Db	329	CACCTGTGCCACAGGGGCTTCCACTGTGACGTGAGCGAGGGGAGATCCATGCTTCAAGATCA	388
Qy	361	GGTACACATCTCGGGGGTGCATTCACAGTGCCTGATAGTCAGTTGCAATGCGCGACTTC	420
Db	389	GGTACACATCTCGGGGGTGCATTCACAGTGCCTGATAGTCAGTTGCAATGCGCGACTTC	448
Qy	421	TCCACGTCTGTGTTATGTGTCATGTGCTCTGTGGGGTGTCTGCCCATGCCCCAGGCTTCC	480
Db	449	TCCACGTCTGTGTTATGTGTCATGTGCTCTGTGGGGTGTCTGCCCATGCCCCAGGCTTCC	508
Qy	481	TGCTGTAAAGACAGGGTGCATCTGTCTCGACAGGTGCTTCTTGCGACATGTTACACC	540
Db	509	TGCTGTAAAGACAGGGTGCATCTGTCTCGACAGGTGCTTCTTGCGACATGTTACACC	568
Qy	541	CGCTGCATCACACCACAGGGGACCCACCCCGCTGGCAAGAAAGTCCCTGTGCCAGAGACT	600
Db	569	CGCTGCATCACACCACAGGGGACCCACCCCGCTGGCAAGAAAGTCCCTGTGCCAGAGACT	628
Qy	601	AACAGGGCAATGGCCCTTGTCCAGTCTGCTGATGTTCTCGGACGACAGTGTCCGGTCCCT	660
Db	629	AACAGGGCAATGGCCCTTGTCCAGTCTGCTGATGTTCTCGGACGACAGTGTCCGGTCCCT	688
Qy	661	GATGTTTACCTGCTGTGATGCTGCCCGAGTGGGAAGTATGATGCTGTGCCAATGGCCAAAC	720
Db	689	GATGTTTACCTGCTGTGATGCTGCCCGAGTGGGAAGTATGATGCTGTGCCAATGGCCAAAC	748
Qy	721	GGCACCTGCTGCTCCGATCACCTGCACTGTGCTGCCCCCAAGACACTGTGTGACTGATC	780
Db	749	GGCACCTGCTGCTCCGATCACCTGCACTGTGCTGCCCCCAAGACACTGTGTGACTGATC	808
Qy	781	CAGAGTAACTGTGCTTCCCAAGGAAGAGCTTACCAGGACTCTCTACTAAGCTCCCTGCG	840
Db	809	CAGAGTAACTGTGCTTCCCAAGGAAGAGCTTACCAGGACTCTCTACTAAGCTCCCTGCG	868
Qy	841	CACACAGTGGCGATGTGAATGTGACATGGAGGTGAGTGGCCAGATGGGTATACCTGC	900
Db	869	CACACAGTGGCGATGTGAATGTGACATGGAGGTGAGTGGCCAGATGGGTATACCTGC	928
Qy	901	TTCGCTTACAGTGGGGGGCTGGGGCTGTGCTGCTCTTATCCAGAGCTGTGTGCTGTGAG	960
Db	929	TTCGCTTACAGTGGGGGGCTGGGGCTGTGCTGCTCTTATCCAGAGCTGTGTGCTGTGAG	988
Qy	961	GACACATACACTGCTTCTCCCGGGGGTTTACGTGTGACAGCGAAGGGTACTGTGAA	1020
Db	989	GACACATACACTGCTTCTCCCGGGGGTTTACGTGTGACAGCGAAGGGTACTGTGAA	1048
Qy	1021	CAGGGGGCCCAACAGGTGCTGTGATGGAAGGGCCCAAGCTCACCTCAGCTGGCCAGAC	1080
Db	1049	CAGGGGGCCCAACAGGTGCTGTGATGGAAGGGCCCAAGCTCACCTCAGCTGGCCAGAC	1108
Qy	1081	CCACAACTTGAAGAGATGTGCCCTGTGTAATGTCAAGACAGTGTCTCTCCGAT	1140
Db	1109	CCACAACTTGAAGAGATGTGCCCTGTGTAATGTCAAGACAGTGTCTCTCCGAT	1168
Qy	1141	ACCTGCTGCCAATCTACGTTCTGGGAGTGGGGCTGTCTCAATGCCAGAGGCTGTCTGC	1200
Db	1169	ACCTGCTGCCAATCTACGTTCTGGGAGTGGGGCTGTCTCAATGCCAGAGGCTGTCTGC	1228
Qy	1201	TGCTCGACACACAGAGCTGTCCCGCCAGCGATACAGTGTGTAGCTGAGGGGAGTGT	1260

Db	Accession	Version	Keywords	Source	Organism	Reference Authors	Title	Journal	Comment
Db	1491								
Db	1501								
Db	1551								
Db	1561								
Db	1611								
Db	1621								
Db	1671								
Db	1681								
Db	1731								
Db	1741								
Db	1791								
Db	1801								
Db	1851								
Db	1861								
Db	1911								
Db	1921								
Db	1971								
Db	1980								
Db	2030								
Db	2040								
Db	2090								
Db	2111								
Db	2157								
Db	2160								
Db	2170								
Db	2180								
Db	2190								
Db	2200								
Db	2210								
Db	2220								
Db	2230								
Db	2240								
Db	2250								
Db	2260								
Db	2270								
Db	2280								
Db	2290								
Db	2300								
Db	2310								
Db	2320								
Db	2330								
Db	2340								
Db	2350								
Db	2360								
Db	2370								
Db	2380								
Db	2390								
Db	2400								
Db	2410								
Db	2420								
Db	2430								
Db	2440								
Db	2450								
Db	2460								
Db	2470								
Db	2480								
Db	2490								
Db	2500								
Db	2510								
Db	2520								
Db	2530								
Db	2540								
Db	2550								

sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).

FEATURES

Location/Qualifiers

1..2157

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="KAT07521"

/cell_line="KATO III"

/cell_type="signet-ring cell carcinoma"

/note="cloning vector pME18SFL3"

1..2157

misc_feature

/note="highly similar to AF055008 Homo sapiens clone 24720 epithelin 1 and 2 mRNA"

BASE COUNT 399 a 691 c 639 g 428 t

ORIGIN

Query Match 96.0%; Score 2010.8; DB 9; Length 2157;

Best Local Similarity 99.1%; Pred. No. 0;

Matches 2043; Conservative 0; Mismatches 17; Indels 2; Gaps 2;

QY 1 CGCAGCAGACCATGTGGACCTGGTGGTGGCTGGCTTTAACAGCAGGCTGGTGGCT 60
DB 29 CGCAGCAGACCATGTGGACCTGGTGGTGGCTTTAACAGCAGGCTGGTGGCT 88
QY 61 GGAACGGGGGCGCCAGATGGTGCATGCTGCTGGCTGGCTGGCTGGACCCGGAGGA 120
DB 89 GGAACGGGGGCGCCAGATGGTGCATGCTGCTGGCTGGCTGGCTGGACCCGGAGGA 148
QY 121 GCCAGCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 149 GCCAGCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 208
QY 181 CTGGGTGG 240
DB 209 CTGGGTGG 268
QY 241 GTCACAGGACTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 269 GTCACAGGACTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 328
QY 301 CACTGCTGCCACGAGGGGCTTCACATGACAGACGAGGCGATCCCTGCTCCAAAGATCA 360
DB 329 CACTGCTGCCACGAGGGGCTTCACATGACAGACGAGGCGATCCCTGCTCCAAAGATCA 388
QY 361 GGTAAACACATCCGCTGGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 389 GGTAAACACATCCGCTGGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 448
QY 421 TCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 449 TCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 508
QY 481 TCGTGTGAAGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 509 TCGTGTGAAGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 568
QY 541 CGCTGCATCAACCCAGGAGGAGCCACCCCTGGCAAAAGAGCTCCCTGCCAGAGACT 600
DB 569 CGCTGCATCAACCCAGGAGGAGCCACCCCTGGCAAAAGAGCTCCCTGCCAGAGACT 628
QY 601 AACAGGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 629 AACAGGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 688
QY 661 GATGTTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 689 GATGTTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 748
QY 721 GCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780

DB 749 GCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 808
QY 781 CAGAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 809 CAGAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 868
QY 841 CACACAGTGGGGGATGTAATGTACATGAGTGGAGTGGCCAGATGGCTATACCTGCTC 900
DB 869 CACACAGTGGGGGATGTAATGTACATGAGTGGAGTGGCCAGATGGCTATACCTGCTC 928
QY 901 TCCCTCTACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 929 TCCCTCTACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 988
QY 961 GACCATATACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 989 GACCATATACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1048
QY 1021 CAGGGGGCCCAACAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1049 CAGGGGGCCCAACAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1108
QY 1081 CCACAAGCTTTGAAGAGATGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1109 CCACAAGCTTTGAAGAGATGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1168
QY 1141 ACCTGCTGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 1169 ACCTGCTGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1228
QY 1201 TGCCTGGACACACAGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1229 TGCCTGGACACACAGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1288
QY 1261 CAGCGAGAGAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1289 CAGCGAGAGAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1348
QY 1321 TCCCAACCCAGAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1349 TCCCAACCCAGAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1408
QY 1381 TGCCTGGACACAGAGTGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1409 TGCCTGGACACAGAGTGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1468
QY 1441 GATCCCGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1469 GATCCCGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1528
QY 1501 AAGGAAGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
DB 1529 AAGGAAGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1588
QY 1561 AAGGAGTGGTGGTGGGAGAGACATTTCTGCATGATTAACAGACCTGCTGCTGCTGCTGCT 1620
DB 1589 AAGGAGTGGTGGTGGGAGAGACATTTCTGCATGATTAACAGACCTGCTGCTGCTGCTGCT 1648
QY 1621 AACCGACAGGGGTGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
DB 1649 AACCGACAGGGGTGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1708
QY 1681 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
DB 1709 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1768
QY 1741 GCCCGCGCTGGGAGCCGCTTTGAGGAGCCAGCCTTGAGACAGCTGCTGCTGCTGCTGCTGCT 1800
DB 1769 GCCCGCGCTGGGAGCCGCTTTGAGGAGCCAGCCTTGAGACAGCTGCTGCTGCTGCTGCTGCT 1828
QY 1801 GTACTGAAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860

Db	1829	GTACGTACAGACTCTGACAGCCCTCGGGAGACCCCACTGGAGAGTGCCCTGTGCTACAGCCCTC	1888
Qy	1861	CCTAGCACCTCCCTCAACCAAAATTTCTCCCTTGAGCCATTCCTGAGCTGCCATCAGCAT	1920
Db	1889	CTTAGACCTCTCCCTTAACCAAAATTTCTCCCTTGAGCCATTCCTGAGCTGCCATCAGCAT	1948
Qy	1921	GGGAGGTGGGGCTCAATCTAAGGCGCTTCCCTGTGCAGAAAGGGGTGAGCGAAAGCC-	1979
Db	1949	GGGAGGTGGGGCTCAATCTAAGGCGCTTCCCTGTGCAGAAAGGGGTGAGCGAAAGCCA	2007
Qy	1980	CATTACAAAGCTCCCAATCCCTCCCGTTTCACTGAGACCCCTGTGGCAGGTGTTTCCCT	2039
Db	2008	CATTACAAAGCTCCCAATCCCTCCCGTTTCACTGAGACCCCTGTGGCAGGTGTTTCCCT	2067
Qy	2040	ATCCACAGGGGTGTGTGTGTGT 2061	
Db	2068	ATCCACAGGGGTGTGTGTGTGT 2089	
RESULT 7			
LOCUS	AY124489	2124 bp	mRNA linear PRI 14-AUG-2002
DEFINITION	AY124489		Homo sapiens PC cell-derived growth factor (GRN) mRNA, complete cds
ACCESSION	AY124489		
VERSION	AY124489.1		GI:22252939
KEYWORDS			
SOURCE			human.
ORGANISM			Homo sapiens
REFERENCE			Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS			1 (bases 1 to 2124)
TITLE			Lu, R., Tian, C. and Serrero, G.
JOURNAL			PCDGF sequence from lambda phage human Jurkat T cell cDNA library (Clontech)
REFERENCE			2 (bases 1 to 2124)
AUTHORS			Lu, R., Tian, C. and Serrero, G.
TITLE			Direct Submission
JOURNAL			Submitted (20-JUN-2002) Pharmaceutical Sciences, University of Maryland School of Pharmacy, 20 N. Pine St., Baltimore, MD 21201, USA
FEATURES			
source			Location/Qualifiers
gene			1..2124
cds			/organism="Homo sapiens"
			/db_xref="taxon:9606"
			/cell_line="Jurkat"
			1..2124
			/gene="GRN"
			/note="PCDGF"
			19..1800
			/gene="GRN"
			/codon_start=1
			/product="PC cell-derived growth factor"
			/protein_id="AA04026.1"
			/db_xref="GI:22252940"
			/translation="MWTLVSNVVALTGLVAGTRCPDQFCPVACCLDPGGASYSQCRPP
			LIDWMPPTLISRLGPGVDNAHSGAGSCTFTVGTSSCCFPFAVAGGDGHHCCP
			RHGCADGSCFORSNGNSVGAIOCPDSOFECDDPSTCCVWDGSGMCCPMPQASCCED
			RVHCCHPCARCDLVAHTRICPTGTGHPPLAKRIAPARTNRVAALSSVMCCPDARS
			STCEELBSGKTGCCPMRNATCCSHLHCCPDIVCDLIQSFCLSKENATYDILTKLP
			HTDPAVDCMDEVCSPDYEYTCRLDSGAMGCCPFIQAVCEBDHICCPAGFTCDQKGT
			CEQDPHYPMWEKAPAHLSLPDQALRDYVCDNVSSCPSDTCCLSGEMGCCPI
			EAVCCSDHOCISPGGYTCVAGOCORSEIYAGLEKMPARASLSHPRDGDCHTSC
			PVGQCTCSLGGSMACOLPHAVCCEDRHCPCPGATYCNVABSCFEKUYSAQATPL
			ARSHVGYKDYECGEGHFCNDJOTCCCDNRGNMACCFYRQGVCCADNRHCCPAGFCA
			ARGTKLRRERPDADLRDPAIRQLL"
BASE COUNT	377 a	683 c	635 g 429 t
ORIGIN			
Query Match	95.4%	Score 1998:	DB 9: Length 2124;
Best Local Similarity	98.9%	Freq. No. 0;	
Matches 2045; Conservative	0;	Mismatches 15;	Indels 8; Gaps 3;

QY	1	CGCAGCAGACCTATGTGGACCTTGAGTGGGTGGCCCTTAACAGCAGGGCTGGTGGCT	60
Db	7	CGCAGGAGACCACTATGTGACCTTGTAAGTGGGTGGCCCTTAACAGCAGGGCTGGTGGCT	66
QY	61	GGAAAGCGGGTCCCAAGATGTCAGATTGTGGCCCTGTGGCTGCTGGCTGGACCCCGAGGA	120
Db	67	GGAAAGCGGGTCCCAAGATGTCAGATTGTGGCCCTGTGGCTGCTGGCTGGACCCCGAGGA	126
QY	121	GGCAGCTACAGCTGCTGCGCGCCCTTCTGGAAATAATGGCCCAACACATGTGAGAGGCAT	180
Db	127	GGCAGCTACAGCTGCTGCGCGCCCTTCTGGAAATAATGGCCCAACACATGTGAGAGGCAT	186
QY	181	CTGGGTGGCCCTCCAGAGTTGATGCCACAGCTGTGGCCGACACTCTGCATCTTTACC	240
Db	187	CTGGGTGGCCCTCCAGAGTTGATGCCACAGCTGTGGCCGACACTCTGCATCTTTACC	246
QY	241	GTCTAGAGGACTTCACATGTGTGTCGCCCTTTCACAGAGCCGTGGCATGCGGGATGGCCAT	300
Db	247	GTCTAGAGGACTTCACATGTGTGTCGCCCTTTCACAGAGCCGTGGCATGCGGGATGGCCAT	306
QY	301	CACCTCTGCCACAGGGGGTTCCATGTGAGTGCAGAGAGGGGGATCCGCTCCAAAGATCA	360
Db	307	CACCTCTGCCACAGGGGGTTCCATGTGAGTGCAGAGAGGGGGATCCGCTCCAAAGATCA	366
QY	361	GGTAAACAATCCGTTGGGTGCCATCCAGCTGCCCTGATAGTCAATTGGAATGCCGAGCTTC	420
Db	367	GGTAAACAATCCGTTGGGTGCCATCCAGCTGCCCTGATAGTCAATTGGAATGCCGAGCTTC	426
QY	421	TCCACGTCTGTTTATGTGTGATGGCTCTCGGGGGTGTGCCCCATGCCCCAGGCTTTC	480
Db	427	TCCACGTCTGTTTATGTGTGATGGCTCTCGGGGGTGTGCCCCATGCCCCAGGCTTTC	486
QY	481	TGCTGTGAAGAAGAGGGTGCATGCTGTGCGCAGAGGTGCGCTTCMGGGACCTGGTTACACC	540
Db	487	TGCTGTGAAGAAGAGGGTGCATGCTGTGCGCAGAGGTGCGCTTCMGGGACCTGGTTACACC	546
QY	541	CGCTGCATCACACCCACAGGGGACCCACCCCTGGCAAAAGCTCCCTGCCCCAGAGACT	600
Db	547	CGCTGCATCACACCCACAGGGGACCCACCCCTGGCAAAAGCTCCCTGCCCCAGAGACT	606
QY	601	AACAGGGCAGTGGCCCTTGTCCAGTCCGTCATGTGTCCGAGCAGCAGGTCCCGGTGCTT	660
Db	607	AACAGGGCAGTGGCCCTTGTCCAGTCCGTCATGTGTGTCCGAGCAGCAGGTCCCGGTGCTT	666
QY	661	GATGGTTTACTCTGTGAGAGCTGCCAGTGGGAATATAGGCGTGCCTCAATGGCCAAC	720
Db	667	GATGGTTTACTCTGTGAGAGCTGCCAGTGGGAATATAGGCGTGCCTCAATGGCCAAC	726
QY	721	GGCAGCTCTGCTCCGATCACTGTGCATGTGTGCCCCCAAGACACTGTGTGACCTGATC	780
Db	727	GGCAGCTCTGCTCCGATCACTGTGCATGTGTGCCCCCAAGACACTGTGTGACCTGATC	786
QY	781	CAGAGTAAAGTCTCTCCAAAGAGAGACGCTACCAGGACCTCCTCACTAAGCTGCTCGC	840
Db	787	CAGAGTAAAGTCTCTCCAAAGAGAGACGCTACCAGGACCTCCTCACTAAGCTGCTCGC	846
QY	841	CACACAGTGGGCGAATGGAATGCAATGAGATGAGTAGTGGCCCAAGATGGCATATCCGCG	900
Db	847	CACACAGTGGGCGAATGGAATGCAATGAGATGAGTAGTGGCCCAAGATGGCATATCCGCG	906
QY	901	TGCCCTTACAGTGGGGGGCTGGGGCTGCTGCCCTTTTACCAGAGCTGTGTGCTGTAG	960
Db	907	TGCCCTTACAGTGGGGGGCTGGGGCTGCTGCCCTTTTACCAGAGCTGTGTGCTGTAG	966
QY	961	GACCACTATCACTGCTCTCCCGCGGGGTTTACGTGTGACACGCAGCAAGGGTACCTGTGAA	1020
Db	967	GACCACTATCACTGCTCTCCCGCGGGGTTTACGTGTGACACGCAGCAAGGGTACCTGTGAA	1026
QY	1021	CAGGGGGCCCCACAGGTGGCTTGGATGTGGAAGGGCCCCAGCTCACCTCAGCTTGCACAGC	1080
Db	1027	CAGGGGGCCCCACAGGTGGCTTGGATGTGGAAGGGCCCCAGCTCACCTCAGCTTGCACAGC	1086

LOCUS	SEQUENCE	3 FROM PATENT	US 5965723	DEFINITION
1081	CCACAAGCCTTGAAGAGAGTGTCCCGCTGATATATGACACAGTGTCCCTCCGCAT	1140		
1087	CCACAAGCCTTGAAGAGAGTGTCCCGCTGATATATGACACAGTGTCCCTCCGCAT	1146		
1141	ACCTCTGCCAACTACACTCTGGGAGATGGGGCTCTCTCCAAATCCAGAGCTGTGC	1200		
1147	ACCTCTGCCAACTACACTCTGGGAGATGGGGCTCTCTCCAAATCCAGAGCTGTGC	1206		
1201	TGCTTGGACACACAGACACTGTCTGGCCCCCAGGATACACAGTGTAGCTGAGGGGACGTGT	1260		
1207	TGCTTGGACACACAGACACTGTCTGGCCCCCAGGATACACAGTGTAGCTGAGGGGACGTGT	1266		
1281	CAGCAGAGAGACGAGATGTGTGGTGTGACTGTGAGAGAGATGCTGCCCGCGGTTCCTTA	1320		
1287	CAGCAGAGAGAGAGATGTGTGGTGTGACTGTGAGAGAGATGCTGCCCGCGGTTCCTTA	1326		
1321	TGCCACCCAGAGATGTGGGTGTGATACAGACACACACTGTCCCGGTGGGGGAAACGTGC	1380		
1327	TGCCACCCAGAGATGTGGGTGTGATACAGACACACACTGTCCCGGTGGGGGAAACGTGC	1386		
1381	TGCCCGAGCCAGAGGTGGGAGCTGGGGCTGTGCCAGTTCGCCCATGTGTGTGTGCAG	1440		
1387	TGCCCGAGCCAGAGGTGGGAGCTGGGGCTGTGCCAGTTCGCCCATGTGTGTGTGCAG	1446		
1441	GATGCCAGACACTGTGTGCCCGGTGTGACTACACACTGTGAAAGAGCTGTGTGTGCAG	1500		
1447	GATGCCAGACACTGTGTGCCCGGTGTGACTACACACTGTGAAAGAGCTGTGTGTGCAG	1506		
1501	AAGGAAGAGGTGTGTGCCCGGTGTGACTACACACTGTGAAAGAGCTGTGTGTGCAG	1560		
1507	AAGGAAGAGGTGTGTGCCCGGTGTGACTACACACTGTGAAAGAGCTGTGTGTGCAG	1566		
1561	AAGGACGTGAGATGTGGGGAAGACACTTCTGCCATGATTAACACAGACCTGTGTGCAGAC	1620		
1567	AAGGACGTGAGATGTGGGGAAGACACTTCTGCCATGATTAACACAGACCTGTGTGCAGAC	1626		
1621	AACGACAGAGGCTGGGCTGTGTCTCTACAGCCAGGCGTGTGTGTGTGTGTGTGTGTGT	1680		
1627	AACGACAGAGGCTGGGCTGTGTCTCTACAGCCAGGCGTGTGTGTGTGTGTGTGTGTGT	1686		
1681	CACCTGTGCTGT	1740		
1687	CACCTGTGCTGT	1746		
1741	GCCCGGCGCTGGGAGAGCCCTTTGAGGAGACAGCTTGAAGAGCTGTGTGTGTGTGTGT	1794		
1747	GCCCGGCGCTGGGAGAGCCCTTTGAGGAGACAGCTTGAAGAGCTGTGTGTGTGTGTGT	1806		
1795	GCGACACTGATGAGACTGTGTGAGCCCTGTGGAGACCCACTGTGAGAGGTGCCCTGTCTCA	1854		
1807	GCGACACTGATGAGACTGTGTGAGCCCTGTGGAGACCCACTGTGAGAGGTGCCCTGTCTCA	1866		
1855	GCGCCTCCCTAGACCTTCCCTTAAACAAATTCCTCTGGAGCCCATTTCTGAGCTCCCAT	1914		
1867	GCGCCTCCCTAGACCTTCCCTTAAACAAATTCCTCTGGAGCCCATTTCTGAGCTCCCAT	1926		
1915	CACCAATGGAGGTGGGCTCAATCTTAAGGACCTTCCCTGTGAGAGAGGGGTGTGAGCA	1974		
1927	CACCAATGGAGGTGGGCTCAATCTTAAGGACCTTCCCTGTGAGAGAGGGGTGTGAGCA	1985		
1975	AAGCC-CATTACAGAGCTCCATCCCTCCCGTTTCACTGAGACCCCTGTGTGTGTGTGT	2033		
1986	AAGCCATTTACAGAGCTCCATCCCTCCCGTTTCACTGAGACCCCTGTGTGTGTGTGT	2045		
2034	TTTCCCTATCCACAGAGGT	2061		
2046	TTTCCCTATCCACAGAGGT	2073		

ACCESSION	AR079655
VERSION	AR079655.1
KEYWORDS	GI:10006396
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 1779)
TITLE	Shoyab,M. and Plozman,G.D.
JOURNAL	DNA encoding epithelins
FEATURES	Patent: US 5965723-A 3 12-OCT-1999;
source	Location/Qualifiers 1..1779 /organism="unknown"
BASE COUNT	304 a 578 c 547 g 350 t
ORIGIN	
Query Match	83.8%; Score 1756.6; DB 6; Length 1779;
Best Local Similarity	99.2%; Pred. NO. 0;
Matches 1765; Conservative	0; Mismatches 14; Indels 0; Gaps 0;
OY	13 ATGTGACCCTGGTGTAGTGAGTGCGGTCCTTAACACAGCAGGGCGTGGTGGGAACGCCGGTGC 72
Db	1 AATGTGACCCTGGTGTAGTGAGTGCGGTCCTTAACACAGCAGGGCGTGGTGGGAACGCCGGTGC 60
OY	73 CCAGATGGTCAGTTCTGCCCTGTGTGGCCCTGTGCTGTGACCCCGAGGAGCACAGCTAACAGC 132
Db	61 CCAGATGGTCAGTTCTGCCCTGTGTGGCCCTGTGCTGTGACCCCGAGGAGCACAGCTAACAGC 120
OY	133 TGCCTGCCCTCCCCCTTCTGTGGCAAAATGGGCCCAACAACATGACAGCAGCATCTGGTGGCCCC 192
Db	121 TGCCTGCCCTCCCCCTTCTGTGGCAAAATGGGCCCAACAACATGACAGCAGCATCTGGTGGCCCC 180
OY	193 TGCCAAGTTTGATGCCCACATGCTCTCCGAGCCACTCCTGCATCTTTACGGTCCAGGAGACT 252
Db	181 TGCCAAGTTTGATGCCCACATGCTCTCCGAGCCACTCCTGCATCTTTACGGTCCAGGAGACT 240
OY	253 TCCAATTGCTGCCCCCTTCCACAGAGGCCGTGGCANTGCGGGGATGGCCATCACTGTGCCCA 312
Db	241 TCCAATTGCTGCCCCCTTCCACAGAGGCCGTGGCANTGCGGGGATGGCCATCACTGTGCCCA 300
OY	313 CGGGGCTTTCACATGTGAGTAGACAGCGGGGATTCCTCTTCCAAAAGATCAAGTTAACACTTC 372
Db	301 CGGGGCTTTCACATGTGAGTAGACAGCGGGGATTCCTCTTCCAAAAGATCAAGTTAACACTTC 360
OY	373 GTGGGTGCACATGCATGCGCCATGATAGTACAGTTGCAATGCCCGGACTTTCACACGCGCTGT 432
Db	361 GTGGGTGCACATGCATGCGCCATGATAGTACAGTTGCAATGCCCGGACTTTCACACGCGCTGT 420
OY	433 GTTATGATCGATGAGTCTGCTGGGGGTGCTGCCCCATGCCCCAAGGCTTCTCTGTGTAAAGC 492
Db	421 GTTATGATCGATGAGTCTGCTGGGGGTGCTGCCCCATGCCCCAAGGCTTCTCTGTGTAAAGC 480
OY	493 AGGGTGACACTGCTGTTCGCGACGCTGCTTCTGCGACCTGTTCACACCCCGCTGATTCACA 552
Db	481 AGGGTGACACTGCTGTTCGCGACGCTGCTTCTGCGACCTGTTCACACCCCGCTGATTCACA 540
OY	553 CCCAGAGGGGACCCACCCCTGTGGCAAAAGAAGCTCCCTGGCCACAGAGACTTAACAGGGCAATG 612
Db	541 CCCAGAGGGGACCCACCCCTGTGGCAAAAGAAGCTCCCTGGCCACAGAGACTTAACAGGGCAATG 600
OY	613 GCCATTGTCCAGTCCGTCATGTGTCCGAGACGACAGTCCCGGTGCGCTGATGGTCTTACAC 672
Db	601 GCCATTGTCCAGTCCGTCATGTGTCCGAGACGACAGTCCCGGTGCGCTGATGGTCTTACAC 660
OY	673 TGCCTGTGAGCTGCCACGTGGGAAATATGAGCTGCGCCCAATGCCCCAACGCCACCTGTCTGC 732
Db	661 TGCCTGTGAGCTGCCACGTGGGAAATATGAGCTGCGCCCAATGCCCCAACGCCACCTGTCTGC 720
OY	733 TTCGATTCACCTGACATGCTGCGCCCCCAAGAACAATGTGTGTGACCTGTATCCAGATTAAGTGC 792
Db	721 TTCGATTCACCTGACATGCTGCGCCCCCAAGAACAATGTGTGTGACCTGTATCCAGATTAAGTGC 780
OY	793 CTCCTCAAGGAAAGCTATACCAAGGAGCTCCTCATATAGCTGAGCTGGGCTACAGTATGTGGC 852

|||||
Db 781 CTCTCCAGAGAAACCTTCCACAGGACCTCTCCTACCTACCTGCTCCGACACAGAGTGGG 840
QY 853 GATGTGAATGTGACATGTGAGGTGAGCTGCCGATGGGTATACCTGCTGCCGTACAG 912
Db 841 GATGTGAATGTGACATGTGAGGTGAGCTGCCGATGGGTATACCTGCTGCCGTACAG 900
QY 913 TCGGGGGCTGGGGCTGCTGCCCTTTTACCAAGCTGTGTGTGTGAGAGCACATACAC 972
Db 901 TCGGGGGCTGGGGCTGCTGCCCTTTTACCAAGCTGTGTGTGTGAGAGCACATACAC 960
QY 973 TGTCTCTCCCGGGGGTTTACGTGTGACAGCAGAAAGGTACCTGTGTAAACAGGGGCCAC 1032
Db 961 TGTCTCTCCCGGGGGTTTACGTGTGACAGCAGAAAGGTACCTGTGTAAACAGGGGCCAC 1020
QY 1033 CAGGTCTCCCTGATGAGAGAGGCCCCAGCTCACCTGCTGACAGCCACCAAGCCTTG 1092
Db 1021 CAGGTCTCCCTGATGAGAGAGGCCCCAGCTCACCTGCTGACAGCCACCAAGCCTTG 1080
QY 1093 AAGAGAGATGTCTCCCTGTATATATGTACAGAGCTGTCTCTCCCTGATACCTGTCCAA 1152
Db 1081 AAGAGAGATGTCTCCCTGTATATATGTACAGAGCTGTCTCTCCCTGATACCTGTCCAA 1140
QY 1153 CTACACTCTGGGAGAGTGGGGCTCTCTCCATCTCCAGAGGCTGTCTGTCTGGACAC 1212
Db 1141 CTACACTCTGGGAGAGTGGGGCTCTCTCCATCTCCAGAGGCTGTCTGTCTGGACAC 1200
QY 1213 CAGCACTGTGCCCCCAGGAGATACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1272
Db 1201 CAGCACTGTGCCCCCAGGAGCTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
QY 1273 GAGATGT 1332
Db 1261 GAGATGT 1320
QY 1333 GACATGGGT 1392
Db 1321 GACATGGGT 1380
QY 1393 GGTGGAGCTGGGGCTGCTGCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1452
Db 1381 GGTGGAGCTGGGGCTGCTGCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
QY 1453 TGT 1512
Db 1441 TGT 1500
QY 1513 TGT 1572
Db 1501 TGT 1560
QY 1573 TGT 1632
Db 1561 TGT 1620
QY 1633 TGT 1692
Db 1621 TGT 1680
QY 1693 GGTGGGT 1752
Db 1681 GGTGGGT 1740
QY 1753 GACGGCCCTTTGAGGAGCCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1791
Db 1741 GACGGCCCTTTGAGGAGCCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1779

VERSION I11830.1 GI:909273
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1779)
AUTHORS Shoyab,M. and Plowman,G.D.
TITLE Epithelins: novel cysteine-rich growth modulating proteins
JOURNAL Patent: US 5416192-A 3 16-MAY-1995;
FEATURES Location/Qualifiers
source 1.1779
BASE COUNT 304 a 578 c 547 g 350 t
ORIGIN
Query Match 83.8%; Score 1756.6; DB 6; Length 1779;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 13 ATGTGACCTGTGTGAGCTGGGTGGCTTTACAGAGAGGCTGTGTGTGTGTGTGTGTGTGT 72
Db 1 ATGTGACCTGTGTGAGCTGGGTGGCTTTACAGAGAGGCTGTGTGTGTGTGTGTGTGTGT 60
QY 73 CCAGATGT 132
Db 61 CCAGATGT 120
QY 133 TGT 192
Db 121 TGT 180
QY 193 TGT 252
Db 181 TGT 240
QY 253 TGT 312
Db 241 TGT 300
QY 313 TGT 372
Db 301 TGT 360
QY 373 TGT 432
Db 361 TGT 420
QY 433 TGT 492
Db 421 TGT 480
QY 493 TGT 552
Db 481 TGT 540
QY 553 TGT 612
Db 541 TGT 600
QY 613 TGT 672
Db 601 TGT 660
QY 673 TGT 732
Db 661 TGT 720
QY 733 TGT 792
Db 721 TGT 780
QY 793 TGT 852

Db	781	CTCTCAAGGAAACGCTACCAACGACCTCTCTACTAAGCTGCTCGCGACACAGTGGAGG	840
Qy	853	GATGTGAATATGTGACATGTGAGAGTGTAGCTGTGCCAGATGTGCTATCTGCTGCCGTATACAG	912
Db	841	GATGTGAATATGTGACATGTGAGAGTGTAGCTGTGCCAGATGTGCTATCTGCTGCCGTATACAG	900
Qy	913	TGGGGGGGCTGGGGGTGTGCTGCCCTTTTACGCCAGAGGTGTGTGCTGTGAGAGCCACTATAC	972
Db	901	TGGGGGGGCTGGGGGTGTGCTGCCCTTTTACGCCAGAGGTGTGTGCTGTGAGAGCCACTATAC	960
Qy	973	TGCTGTCCCGGGGGTTTACGTGTGACACGACGAAGAGGTACTCTGTGTGAACAGGGGCCAC	1032
Db	961	TGCTGTCCCGGGGGTTTACGTGTGACACGACGAAGAGGTACTCTGTGTGAACAGGGGCCAC	1020
Qy	1033	CAGGTGCCCCGTGATGTGACAAAGAGGCCCACTACCTTCACCTGTCCAGACCCACAACTTGG	1092
Db	1021	CAGGTGCCCCGTGATGTGACAAAGAGGCCCACTACCTTCACCTGTCCAGACCCACAACTTGG	1080
Qy	1093	AAGAGAGATGTCTCCCTGTGATTAATGTACAGACGTCTCCCTCTCCGATACCTGCTGCCAA	1152
Db	1081	AAGAGAGATGTCTCCCTGTGATTAATGTACAGACGTCTCCCTCTCCGATACCTGCTGCCAA	1140
Qy	1153	CTCACGTCTGGGGAGTGGGGGCTGTGTCCAAATCCAGAGGCTGTGTCTGTGGAGCAC	1212
Db	1141	CTCACGTCTGGGGAGTGGGGGCTGTGTCCAAATCCAGAGGCTGTGTCTGTGGAGCAC	1200
Qy	1213	CAGCACTGCTGCCCCCACCACGATATACACGTGTGTAGCTGTGAGGGGCACTGTACAGAGAAAGC	1272
Db	1201	CAGCACTGCTGCCCCCACCACGATATACACGTGTGTAGCTGTGAGGGGCACTGTACAGAGAAAGC	1260
Qy	1273	GAGATCTGTGGCTGTGACTGTGAGAAAGATGGCTGCCGCCCGAGTTCCTTTATCCACCCAGA	1332
Db	1261	GAGATCTGTGGCTGTGACTGTGAGAAAGATGGCTGCCGCCCGAGTTCCTTTATCCACCCAGA	1320
Qy	1333	GACATCGGCTGTGACACACACACACAGCTGTGCCGTGGGGCGGAACCTGTGCCCGAGCCAG	1392
Db	1321	GACATCGGCTGTGACACACACACACAGCTGTGCCGTGGGGCGGAACCTGTGCCCGAGCCAG	1380
Qy	1393	GGTGGGACCTGGGCTGTGCTGTGCACATGTGGCCCATGCTGTGTGTGTGGGAGATGCCAGCAC	1452
Db	1381	GGTGGGACCTGGGCTGTGCTGTGCACATGTGGCCCATGCTGTGTGTGTGGGAGATGCCAGCAC	1440
Qy	1453	TGCTGCCCGGGTGTGTACACCTGTCAACGTGAAGGCTCATCTGTGAGAGAAAGATGTGTC	1512
Db	1441	TGCTGCCCGGGTGTGTACACCTGTCAACGTGAAGGCTCATCTGTGAGAGAAAGATGTGTC	1500
Qy	1513	TCTGTCCACAGCTGCCACACTTCTGTGGCCCGGTAGCCTCAAGTGGGTGTGAAGAGCTGGAG	1572
Db	1501	TCTGTCCACAGCTGCCACACTTCTGTGGCCCGGTAGCCTCAAGTGGGTGTGAAGAGCTGGAG	1560
Qy	1573	TGTGGGGAAGGACATTTGTGGCATATATTAACGACGACTGTGTGCGGAGACAAACCGAAGGGC	1632
Db	1561	TGTGGGGAAGGACATTTGTGGCATATATTAACGACGACTGTGTGCGGAGACAAACCGAAGGGC	1620
Qy	1633	TGGGCTACTGTCTCCCTACAGCCAGAGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1692
Db	1621	TGGGCTACTGTCTCCCTACAGCCAGAGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1680
Qy	1693	GCTGTCTTCCTGTGCGCACGACGAGGGGTACCAAGTGTGTGTGCGAGGAGGAGGCCCGGCTGG	1752
Db	1681	GCTGTCTTCCTGTGCGCACGACGAGGGGTACCAAGTGTGTGTGTGCGAGGAGGAGGCCCGGCTGG	1740
Qy	1753	GACGCCCTTTGAGGAGACCAACGCTTTGAGAGACGCTGCG	1791
Db	1741	GACGCCCTTTGAGGAGACCAACGCTTTGAGAGACGCTGCG	1779

RESULT 10	AK023348	AK023348	AK023348	AK023348
LOCUS	1630 bp	mRNA	linear	PRI 01-AUG-2002
DEFINITION	Homo sapiens CDNA FLJ13286 fts, clone OVARC1001154,			highly similar
ACCESSION	to Homo sapiens clone 24720 epithelin 1 and 2 mRNA.			
	AK023348			

KEYWORDS	AK023348.1 GI:10435243
VERSIONS	Cligo capping, fis (full insert sequence).
SOURCE	Homo sapiens ovary, tumor tissue cDNA to mRNA, clone:OVARC1 clone:OVARC1001154.
ORGANISM	Homo sapiens
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	1 Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sato,H., Sugano,S., Shiratori,A., Sudo,H., Wagaatsuma,M., Hosoi,T., Kaku,Y., Kodaira,H., Kondo,K., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuno,Y., Niimiya,K. and Iwayanagi,T.
TITLE	NEDO human cDNA sequencing project
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1630)
AUTHORS	Isogai,T. and Otsuki,T.
TITLE	Direct Submission
JOURNAL	Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0012, Japan (E-mail:genomics@helix.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan: cDNA full insert sequencing: Research Association for Biotechnology: cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
COMMENT	
FEATURES	
SOURCE	Location/Qualifiers
	1..1630
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="OVARC1001154"
	/tissue_type="ovary, tumor tissue"
	/clone_1ib="OVARC1"
	/note="cloning vector: PME18SFL3"
	85..1326
	/note="unnamed protein product"
	/codon_start=1
	/protein_id="BAB14535.1"
	/db_xref="GI:10435244"
	/translation="MATTAAGASTAVOTGDPADQVTPWPVSSALIYSSNRTSP RAVLSMAPGAAPCPRLPAVKTGCTACDLIOSKMSKEATTDILTKLPAHVGVN KCMDEVSADPSYTCRCRLOSAGMGCCPTCAOEDHJHCPAGTCTPMOKCTCGGRR OYPMERKAPAHLSLPDQALAKRDVPDNNVSSPESDTCQLTSEWKCCLPEAVGCTC DHQGCQPGITCVAEGGCCQRGSEITVAGLEKPARASLSHPRIDGCDQNSCPVGQTC CPISGSGSWACCCDPAHVCEDRCHCCPAGYCNVKNARCEEVSAQPAFTLASPVHV GVKVSGWCEGEGHCHDNOTCCRDNRQNAACPYRQGVCCADBRHCCPAGFRCARGTCKC LRREAPRMDAPLRDPAALROLL"
	297..298
	/note="260 bases segment is present in AF055008, X62320 and AK000607."
BASE COUNT	285 a 517 c 489 g 339 t
ORIGIN	
Query Match	60.7%; 1271.2; DB 9; Length 1630;
Best Local Similarity	84.9%; Pred. No.7.9e-268;
Matches 1574; Conservative	0; Mismatches 18; Indels 262; Gaps 3;
OY	209 ACTGCTCTGCGGGCCACATCTGCATCTTTACCGTCTCAGGAGCATTCAGTTGCTGCCCT 268
Db	1 ACTGCTCTGCGGGCCACATCTGCATCTTTACCGTCTCAGGAGCATTCAGTTGCTGCCCT 60
OY	269 TCCAGAGGCGGTGGCATGCGGGGATGGCCATCACTGCTGCCACGGGGCTTCCACTGCA 328
Db	61 TCCAGAGGCGGTGGCATGCGGGGATGGCCATCACTGCTGCCACGGGGCTTCCACTGCA 120
OY	329 GTGCAGAGCGGGGATCTGCTCCAAAAGTCAAGTAAACAAGTCCTGGGTGCATTCAGT 388
Db	121 GTGCAGAGCGGGGATCTGCTCCAAAAGTCAAGTAAACAAGTCCTGGGTGCATTCAGT 180

QY	1501	AAGGATGAGGCTCTGCGCCAGCCCTGACACCTTCTCGGCCGCGAAGCCCTACCTGGGGTGG	1560
Db	1513	AAGGATGCAAGGCTCTGTGTCCAGCCCTTCCATGGACCTGACCTTTGGCTCTAAGGTTGG----	1568
QY	1561	AAGGACGTGGAGTGTGGGGAAAGGACACTTCTGCGCATGATTAACGACAGCTGTGCGCGAGAC	1620
Db	1569	--GANTGTGGATATGTGGTCCGGACATTTCTGCGCATGATTAACGACAGCTGTGTGTAAGAG	1626
QY	1621	AACCGACAGGGCTGGGGCTGCTGTCTCCCTTAACGCCAGGGCGCTGTGTTGTCTATGCGGCG	1680
Db	1637	AGCCAAAGAGGCTGGGGCTGCTGTCTCCATGTAAGAAAGGGTGTCTGCTGTAGAGATGACGCT	1686
QY	1681	CACCTCTGNCCTGCTGGGCTCCGCTCCGCGACAGCAGAGGGGAGACCAAGTGTGGCGAGGGG	1740
Db	1687	CACCTTGTGCCATTGTGGCTTGCACCTGTTCAGCCAAAGGACCAAGTGTGTGGGAAGAG	1746
QY	1741	GCCCCGCGCTGGGAGCCCGCTTTGAGGGAGACCCAGCGCTTGAGACAGCTGCTGTGAGG----	1796
Db	1747	ACCCCCTGCTGGGACATATTGTTGAGGGATCCAGGCCCAAGACCGCTACTGTGAGGAAGG	1806
QY	1797	--GACAGTACTGAGACTCTGACAGCCCTTGGGGAGCCCCACTGTGGAGGGTCCCTGTGCTCA	1854
Db	1807	GCTAACGACTAAAGAACTCCACAGTCCGTGGGAACCGCTGTCTGAGGGGATATCCACCACTCA	1866
QY	1855	GACCCCTCCAGACCTCCCGCTTAACCAAAATTCCTGTGAGACCCCAATTCGAG--CTCCCCA	1913
Db	1867	GCGCTCCCTGGCACCTCTTCT--TTACTGTCTCCCGCGCTACTCTTCTGATCAACCCCA	1924
QY	1914	TCACCATGGAGGTGGGGCTTCATCTAAGGCCCTTCCCTGTCAAGAAAGGGGGTTAGGCA	1973
Db	1925	TCACCATGGAAGGTGGGGCTCAAACTTAAGACCTCTCTTAAGGAAAGGAGCTGTGGGA	1984
QY	1974	AAAGCCCATTCAGACTGCCATCCCTCCCGCTTTCAGTGAACCCCTGTGGCCAGGTGCTT	2033
Db	1985	AAAGCCCGCTATCAAACTGCATTCTTCTGATTTCTGTGGACCTTGTGGCCAGGTGCTC	2044
QY	2034	TTCCCTATCCACAGGGGTGTGTGTGTGGGTGG	2069
Db	2045	TTTCGATCCACAGGTGTGTGTGTGTGAGCTTGCCTTTGG	2080

Db	427	GCTGTATTAATGATATGATGGTTCTGTGGGGTGTCTGCCATATGCCAAGGCTCTGTCTGGT	486
OY	488	AAGACAGGGGTGCACACTGCTCTCGGCACGGGTGCTCTCGACTGTGTTACACACCCTGTGA	547
Db	487	AAGACAGAGTGCATTTGCTGTCCCAAGGGGCTCTCTGTGACCTGTTCACACCCGATGA	546
OY	548	TTCAACCCAGGGGACCCACCCCTTACTAAATAATTTCCCGACAAAGACCAACAGGG	606
Db	547	TTTACCCAGGGGACCCACCCCTTACTAAATAATTTCCCGACAAAGACCAACAGGG	606
OY	608	CAGTGGCCTTGTCCAGCTGGGTGATGTGACCGAGACACAGGTCCCGGTCTGATGGTT	667
Db	607	CAGTGGC---TTTCCTTTTCCGTGTGTGGCTGTGGCTGATGCTTAAGCACCCAGTCCCTGATACT	663
OY	668	CTACCTGCTGTGAGCTGTGCCAGTGGGAATATAGCTGTGTGGCCCATGTGCCCAAGCCCACT	727
Db	664	CTACCTGCTGTGAGCTGTGCCAGTGGGAATATAGCTGTGTGGCCCATGTGCCCAAGCCCACT	723
OY	728	GCTGCTCGATACACTGTGACATGTGCCCCAAGACACTGTGTGACCTGATCCGATGA	787
Db	724	GCTGTTCACACACTGTGACATGTGCCCCAAGACACTGTGTGACCTGATCCGATGA	783
OY	788	AGTGCCTTCCAAAGAGAAAGCTACACAGGACCTCCACTAATGCTGCTGCGCACAG	847
Db	784	AGTGCATTTCCAAAGACTAC---ACCACAGATCTATGACCAAGCTGCTGATACCCAG	840
OY	848	TGGGCGATGTGAATGTGACATGAGATGAGCTGCCAGATGGCTATACCTGTGCTGCATC	907
Db	841	TGAATGTGAGGAATGTCGACTTGGAGTGTGATGCTCATGCTCAACTGCTGCTCCGCC	900
OY	908	TACAGTGGGGGGCTGGGGCTGCTGCCCTTTTACCCAGGCTGTGTGCTGTGAGGACACA	967
Db	901	TCAACACTGGGGGGCTGGGGCTGCTGCTCCATTACCAAGGCTGTGTGTGAGAGACACA	960
OY	968	TACACTGCTGTCCCGCGGGGTTTACGTGTGACACGCAAGGATPACCTGTTGAACAGGGGC	1027
Db	961	TTCACTGCTGTCCCGCGGGGTTTACGTGTGACACGCAAGGATPACCTGTTGAACAGGGAG	1020
OY	1028	CCCAACAGGTGCTCTGTATGGAAGGCCCCCACTCACTCACTGCTGCCAAGCCACAG	1087
Db	1021	TCCTTCAGGTACCCCTGTGATGAATAAGGTCAAGGCTCCCTCAAGCTGTGCAGACCCACAGA	1080
OY	1088	CCCTGAAGAGATGTCCCTGTGATGAATGTCAAGCAGCTGTCCCTTCGATACCTGCT	1147
Db	1081	TCCTGAAGATATGTCCCTGTGATGAATGTCAAGCAGCTGTCCCTTCGATACCTGCT	1140
OY	1148	GCCCACTCACGTGTGGGAGTGGGAGCTCTGTCCAAATCCAGAGCTGTCTGCTGTGG	1207
Db	1141	GCAAGCTCACTTGTGGGACTGTGGGCTCTGTCCCAATGCCAGAGCTGTCTGCTGTAG	1200
OY	1208	ACCACAGCACTGCTGCCCCAGCAGATACAGTGTGTAGCTGAAGGGGCACTGTCAACGAG	1267
Db	1201	ACCACAGCACTGCTGCCCCAGCAGATACAGTGTGTAGCTGAAGGGGCACTGTCAACGAG	1260
OY	1268	GAAAGAGATGTGGGGGAGCTGAGATGAATAGCTGCCCCGCGGGTTCCTTATCCAC	1327
Db	1261	GAGAGAGATGTGGGGGAGCTGAGATGAATAGCTGCCCCGCGGGTTCCTTATCCAC	1320
OY	1328	CCAGAGACATGGCTGTGACACAGACACACAGCTGCCCGGTGGGCGGAACCTGTGCCGA	1387
Db	1321	ATGGAGATATTTGTGTGTGACACAGATACACAGCTGCCCAATAGGGCAACATGTGCCAA	1380
OY	1388	GCCAGAGGTGGGAGCTGGGCGCTGTGCCAGTTGGCCCCATGCTGTGTGTGTGAGAGACCGC	1447
Db	1381	GCCAGAGGTGGGAGCTGGGCGCTGTGCCAGTTGGCCCCATGCTGTGTGTGTGAGAGACCGC	1440
OY	1448	AGCACTGTGCCCCGCTGGCTGAACCTGTCAACAGTGAAGGAGGATG	1507
Db	1441	AGCACTGTGCCCCGCTGGCTGAACCTGTCAACAGTGAAGGAGGATG	1500
OY	1508	TGGTCTGTGCGACCTGTGCACTTCTTGGCCGTACCTCAACGTGGGTGAAGAGACG	1567

Db	1501	CAGGCTGTGCCAGCCTTCCATGACACTGACCCTTTGGCTTAAGGTTGG-----GAATG	1554		
Oy	1568	TGAGTGTTGGGAGAAGACACTTTCGCATGATAAACAGACTGTGCGGACACAACCGAC	1627		
Dd	1555	TGGAATGTGGGCGCGGCATTTCCTGCATGATAAACCAAGTCCGTGTTAATAAGCCGAG	1614		
Oy	1628	AAGGCTGGGCGCTGTGTGCCCTTACGCCAGGCGCTGTGTGTCTCATATCGGGCCACGTGCT	1687		
Dd	1615	GAGGCTGGGCGCTGTGTGCCCTTACGCATGATAAAGGTTGTGTGTGATGAGATGACGTCTGT	1674		
Oy	1688	GTCTGTGTGGCTTCOCGTGCGCACGACGAGGGGTACCAAGTTTTGGCGACAGAGCCCCGC	1747		
Dd	1675	GTCCCATTTGGCTTCACACTGTTCACGCAAGGAAACCAATGTTTTGGCGAAGAACCCCTC	1734		
Oy	1748	GCTGGAGACGCCCTTTGAGGGAGCCAGCAGCTTGAGACAGCTGCTGTGAG-----GACAG	1801		
Dd	1735	GCTGGAGACATTTTGTAGGGATCCAGGCCCAACAGCCGTACTGTGTAGGAAGGCTTACG	1794		
Oy	1802	TACTGAAGACTGTGACGCCCTTGGGACCCCACTGGAGGGGAGCCCTGTGCTCAGGCCCTC	1861		
Dd	1795	ACTTAAGAACTCCACAGCTCTGGAAACCTGTTCTGABGGTATCCACACTCAGGCTCC	1854		
Oy	1862	CTACACACTTCCCCTTACCAAATTTCTCCCTGAGCCCACTTGTAG-CTCCCATCAACAT	1920		
Dd	1855	CTGACACTTCTTCT--TTAGTCTCCCGCGGCTACTCATTTGTGAGTACACCCATCACAT	1912		
Oy	1921	GGAGGTGGGAGCCCTCAATCATAGGCCCTTCCCTGTACAGAGGAGGTTTAGGCANAAAGCCC	1980		
Dd	1913	GGAAGTGGGGCCCTCAACATCAAGCCTTCTTATGAAAAGAAAGGCTGTGGCAAAAGCCC	1972		
Oy	1981	ATTACAGCTGCCATCCCTTCCCGTTCAGTGGACCCGTGGCCAGTGCCTTTTCCCTA	2040		
Dd	1973	CGTATCAAACTGCCATTTCTTATGATTTCTGTGACCTTGTGGCCAGGTGCTTCTCGA	2032		
Oy	2041	TCCACAGGGGTGTGTGTGTGTGTGGGTG	2069		
Dd	2033	TCCACAGGTGTGTGTGTGTGTGTGGT	2061		
RESULT 13	MUSAG	2125 bp	mRNA	linear	ROD 01-JUL-1993
LOCUS	Mouse acrogranin mRNA, complete cds.				
DEFINITION	M86736				
ACCESSION	M86736.1 GI:191766				
VERSION	acrogranin; acrosomal glycoprotein.				
KEYWORDS	Mus musculus (Library: lambda-gtlI of T.Baba) male adult testis				
SOURCE	CDNA to mRNA.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.				
TITLE	1 (bases 1 to 2125)				
JOURNAL	Baba,T., Hoff,H.B. III, Nemoto,H., Lee,H., Orch,J., Arai,Y. and				
MEDLINE	Getton,G.L., an acrosomal cysteine-rich glycoprotein, is the				
PUBMED	precursor of the growth-modulating peptides, granulins, and				
FEATURES	epithelins, and is expressed in somatic as well as male germ cells				
source	Mol. Reprod. Dev. 34 (3), 233-243 (1993)				
gene	93228994				
CDS	8471244				
	Location/Oualifiers				
	1..2125				
	/organism="Mus musculus"				
	/db_xref="taxon:10090"				
	/sex="male"				
	/tissue_type="testis"				
	/dev_stage="adult"				
	/tissue_id="lambda-gtlI of T.Baba"				
	1..2125				
	/gene="acrogranin"				
	25..1794				
	/gene="acrogranin"				
	/codon_start=1				

/product="acroganin"
/protein_id="AAA37191.1"
/db_xref="GI:191767"
translation="MVMVMSWIAFAAGVAVAGTCCPDGDFPACCLDGGAGNSCPN
LIDTPRITSHLDGSCOTGHGAGVAGTCTLTGVTGSCCPSPGVSQDGHYHCCPOG
PHCSADKSCFQMSDNPLGAVOCFSGSRECDSDATCCIMVDSMCCMPASCCEDR
VHCCHGASCDLVHRCVSPYTHTLKLPFAQKTRNVSIPFVSVCADATGCPDSD
TCBELPTGKYCCMPNPAICSDHLHCPODLDVIOKCLSKNYTDLTKLPGYP
VKEVCKMEVCSPEBGTCCRLNTGAMGCCPKAVCCEDHHCPCAGQCHETKTC
MGLIOWPMKRVIAPLRDPOLKSDPCCDFTRCPTNNTCCILNSGDMGCPPEA
VCGSDNHCNAGFTCLAGYCKGKDMVALEKIPAROTPLIOGIDGCDHSCPY
GOTCCPSLKSMAACQLEPHAVCCEDRQCCAGTTCNKAATCEKDDPFIOPVILTL
GPKVNEGCGHFCNDQTCDSAGVACCPYLKGVCCCRHRCPCGPHCSARGT
KCLRKRIIPRMDFLNDPVRPL"

519_peptide
/gene="acroganin"
76..1791
mat_peptide
/gene="acroganin"
/product="acroganin"
136..138
misc_feature
/gene="acroganin"
/note="possible asparagine-linked glycosylation site"
811..813
misc_feature
/gene="acroganin"
/note="possible asparagine-linked glycosylation site"
1141..1143
misc_feature
/gene="acroganin"
/note="possible asparagine-linked glycosylation site"
1600..1602
misc_feature
/gene="acroganin"
/note="possible asparagine-linked glycosylation site"
2107..2112
polyA_site
/gene="acroganin"
2125
polyA_site
/gene="acroganin"
432 a 610 c 581 g 502 t

BASE COUNT
ORIGIN

Query Match 58.0%; Score 1214.2; DB 10; Length 2125;
Best Local Similarity 75.8%; Pred. No. 2.2e-255;
Matches 1574; Conservative 0; Mismatches 483; Indels 20; Gaps 5;

QY 1 CCGAGGACACCATGTGACCTGTGAGCTGGTGCCCTTAACAGCAGGCTGTGCT 60
DB 13 CCGAGGACACCATGTGAGCTGGTGCCCTTAACAGCAGGCTGTGCT 72
QY 61 GGAAGCGGCGCCAGATGATGCTGCTGAGCCCTGCTGCTGAGCCCGGAGGA 120
DB 73 GGAAGCGGCGCCAGATGATGCTGCTGAGCCCTGCTGCTGAGCCCGGAGGA 132
QY 121 GCGACGTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 133 GCGACGTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 192
QY 181 CTTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 193 CTTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 252
QY 241 GCTCAGGAGCTTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 253 GCTCAGGAGCTTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 312
QY 301 CACTGCTGCCAGGAGCTTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 313 CACTGCTGCCAGGAGCTTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 372
QY 361 GGTAAACAACTCCGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 373 G---ATAACCCCTTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 429
QY 421 TCCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 430 GCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 489

QY 481 TCCGTGGAAGACAGGAGTGCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 490 TCCGTGGAAGACAGGAGTGCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 549
QY 541 CCGTGCATCACACCCAGGAGCACCACCCCTGCGCAAGAAAGACTCCCTGCGCAGAGACT 600
DB 550 CCGTGCATCACACCCAGGAGCACCACCCCTGCGCAAGAAAGACTCCCTGCGCAGAGACT 609
QY 601 AACAGGAGAGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 610 AACAGGAGAGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 669
QY 661 GATGTTTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 670 GATGTTTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 729
QY 721 GCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 730 GCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 789
QY 781 CAGAGTAAAGTGCCTGCCAAGAGAACGCTACACGAGACCTGCTGCTGCTGCTGCTGCTGCT 840
DB 790 CAGAGTAAAGTGCCTGCCAAGAGAACGCTACACGAGACCTGCTGCTGCTGCTGCTGCTGCT 846
QY 841 CACACAGTGGGAGATGTGAATGTGACATGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 900
DB 847 TACCCAGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 906
QY 901 TCCCTGCTACAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGT 960
DB 907 TCCCTGCTACAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGT 966
QY 961 GACCATATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 967 GATCATATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1026
QY 1021 CAGGAGCCCGACACAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1027 ATGGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1086
QY 1081 CCACAAGCTTGAAGAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1087 CCACAAGCTTGAAGAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
QY 1141 ACCTGCTGCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 1147 ACCTGCTGCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1206
QY 1201 TCCCTGAGCACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1207 TCCCTGAGCACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1266
QY 1261 CAGCAGAGAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1267 CAGCAGAGAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1326
QY 1321 TCCCAAGGAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1327 TCCCAAGGAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1386
QY 1381 TCCCAAGGAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1387 TCCCAAGGAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1446
QY 1441 GATCCCAAGGAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1447 GATCCCAAGGAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1506
QY 1501 AAGGAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
DB 1507 AAGGAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1562

Db	131	GCCTACATGAGTGTGCTGTAACCCCTTCTTGAGACACATGCGCTAGAAATACGAGCATCAT	190
QY	121	GCACAGTAAAGCTGCTGCGCTGCCCTCTTGAGACAAATGGCCACCAACACTGAGCAGGCT	180
Db	71	GGACACACATGTCACAGATGGGAGAGTCTGCCCTGTGCTGCTGACCTTACACAGGAGGA	130
QY	61	GGACAGCGGTGCCACAGATGGTCAATTCTGCCCTGTGGCTGTGCTGTGACCCCGGAGGA	120
Db	11	CCGACAGACACATGTGGGTCTCTGATGAGACTGTGGCTTGGCGGACAGGCTGTGTAGCC	70
QY	1	CCGACAGACACATGTGACCTGTGAGACTGGGTGACCTTAAACAGAGGCTGTGGCT	60
Db	11	CCGACAGACACATGTGGGTCTCTGATGAGACTGTGGCTTGGCGGACAGGCTGTGTAGCC	70
QY	1741	ATTTCTGCTGCTGGACATGTTTTTGAGGGATCCGGATCCCAAGACCCCTACTGTAAAGAGG	1800*
QY	1801	GTAACGAA-----GACTGTGACCCGCTCGGAGACCCACATCGGAGGGGCTGTGCTGCTC	1853
Db	1801	GCTACAGACTTAAGAACTCCACAGTCTCTGGAGACCTGTTCGAGGGATCCACTACTCT	1860
QY	1854	AGGCTTCCTTACACACTCCCTCCCTTAAACAAATTCCTCGACCCCACTTCTGAG-CTCC	1912
Db	1861	AGGCTTCCTTACACACTCCCTCCCTTAAACAAATTCCTCGACCCCACTTCTGAGTACCT	1920
QY	1913	ATCACCATGGAGGTGGGGCTCAATCTTAAGGCCCTTCCCTGTCAAGAGGGGTTGAGGC	1972
Db	1921	ATCACCATGGAGGTGGGGCTCAATCTTAAGGCCCTTCCCTGTCAAGAGGGGTTGAGGC	1980
QY	1973	AAAAGCCATTTACAAGCTGCCATTCCTCCCTCCGTTTCAAGTGGACCTGTGGCCAGTGTCT	2032
Db	1981	AAAAGCCATTTACAAGCTGCCATTCCTCCCTCCGTTTCAAGTGGACCTGTGGCCAGTGTCT	2040
QY	2033	TTTTCTATCAACAGAGGGGTGTTGTGTGTGGGTG	2069
Db	2041	CTTCCGAGACCAAGGTGTCTGTGAGCTGTGTG	2077
RESULT 14			
ARI175447		2137 bp	DNA
LOCUS	ARI175447	Sequence 1 from patent US 6309826.	linear
DEFINITION			
ACCESSION	ARI175447		
VERSION	ARI175447.1	GI:17916746	
KEYWORDS			
SOURCE			
ORGANISM		Unknown.	
REFERENCE		Unclassified.	
AUTHORS		1 (bases 1 to 2137)	
TITLE		Serreto,G.	
JOURNAL		88bda tumorigenic growth factor and antagonists	
FEATURES		Patent: US 6309826-A 1 30-OCT-2001;	
	source	1. 2137	
		/organism="unknown"	
BASE COUNT	442 a	613 c	580 g
ORIGIN			502 t
Query Match	57.3%	Score 1200:	DB 6: Length 2137;
Best Local Similarity	75.6%	Pred. No. 2.8e-252;	
Matches 1572; Conservative	0;	Mismatches 485;	Indels 21; Gaps 6;

QY	181	CTGGGTGGCCCTTGGCCAGGTTGATATGCCACTGCTCTGCGGGCACTCTCTCACTTTTACC	240
Db	191	TTATTTT	250
QY	241	GTTCTAGGGGACATTCCAGTTGCTGCTCCCTTCCAGAGGCGGTGGGATGCGGGGATGGCCAT	300
Db	251	TT	310
QY	301	CACCTGTGCCACAGGGGGCTTCCACTGCAATGACAGACGGGGATGCTCTTCCAAAGATTA	360
Db	311	CACCTGTGCCACAGGGGGCTTCCACTGCAATGAGATGGAAATCTCTCCACAGATGTCA	370
QY	361	GGTAAACAATCCGTGGGTGCTATCCAGTGCCTCGATATGTCGATTCGATGCCGGACTTC	420
Db	371	G--ATTAAACCCCTTGGGTGCTATCCAGTGCCTGCGGGACAGTTTGATATCTCGACTCT	427
QY	421	TCCAGCTGCTGTATATATGGTCGATATGCTCTCTGGGGGGTGCCTCCATGCCCAAGGCTTCC	480
Db	428	GCCACTGCTGCAATATATATGGTTATGGTTCTGTGGGGATGTTGTGCCAATGCCCAAGGCTCT	487
QY	481	TGCTGTGAAGACAGAGGTGCACTGCTGTGCCACAGGTCCTTCTGCGACTGTGTACACC	540
Db	488	TGCTGTGAAGACAGAGGTGCAATGCTGTGCCCATATGGGGGCTCTGTGACTGTGTTACACA	547
QY	541	CGTGCATACACACCACAGGGGACCCACCCCTGGCAAAAGACTCCTGTGCCAGAGACT	600
Db	548	CGATGCGTTTACCCACAGGGGACCCACACCCCTACTAAAGAAATTCCTGCAAAAACCC	607
QY	601	AACAGGGCAGTGGCCTTGTCCACTGCGTATATGTCTCGGACGACGAGTCCCGTGGCCT	660
Db	608	AACAGGGCAGTGGCTTGTCCCTTTTCTGTGTGTGCTGACCTATGTTAAGACCAATGTGCC	667
QY	661	GATGTTTCTACGCTGTGTAGTACCACAGTGGGAATGATGGTCTGCCCAATGCCAAC	720
Db	668	GATGATTTCTACGCTGTGTAGTACCACACTGGGAAGATATGGTCTGTCCAAATGCCAAT	727
QY	721	GCCACTGCTGCTCCGATCACTGTCACTGTGCCCAAGACACTGTGTGACTGATC	780
Db	728	GCCATGTGCTTCCGACCACTGTCACTGTGCCCAAGACACTGTATGACTGATC	787
QY	781	CAGATATAGTCCCTTCCAGGAAAGCGTATCCACGAGACCTCCACTAATAGCTGCCGTGC	840
Db	788	CAGATATAGTCCCTTCCAGGAAAGCGTATCCAGGATCTCCGACCAAGCTGCCGTGA	844
QY	841	CACACATGGGCGCATGGAATGTGATGATGAGGTGAGTGCACAGATGGCTATACCTGC	900
Db	845	TACCCAGTGAAGAGGTGAAGTGCAGATATGAGGTGAGTGCCTGAAAGATATACCTGC	904
QY	901	TGCCGTCTACAGTCCGGGGGCTTGGGCTGTGCCCTTTTACCAAGGCTGTGTGCTGTAG	960
Db	905	TGCCGCTTCAACACTGGGGGCTTGGGCTGTGTCATTTGGCAAGGCGTGTGTGTGAC	964
QY	961	GACCAATATACATCTGTGTCCCGGGGTTTACGTGTACACGCAAGAGGTACTGTGAA	1020
Db	965	GATCAATTCATTTGTGCTCCGGGAGGTTTCAAGTGTACACAGGAAAGAACTGTGGAA	1024
QY	1021	CAGGGGCCCCACAGGAGCCCTGGATGAGAGAGGCCCCAGCTCACTCAGCTGCCACAGAC	1080
Db	1025	ATGGGTATCTTCCAGATGAGGTGATAGAGAGGCTCATAGCCCCCTGCTGCCACAGAC	1084
QY	1081	CCACAAGCCTTGAAGAGATGTCCCTGTGATATATCTACAGACTGTCCCTCTCGAT	1140
Db	1085	CCACAAGTCTTGAAGATGATATACACTTGTGTATACCTTCACTAGTGTGTCCTACAAACAAT	1144
QY	1141	ACCTGTGCCCACTACGCTGTGGGAGTGGGGCTGTGTCCAAATCCAGAGGCTGTGTGC	1200
Db	1145	ACCTGTGTCAAACTCAATTTCTGGGAGTGGGGGCTGTGTCCCAATCCAGAGGCTGTGTGC	1204
QY	1201	TGCTGGACACACAGACATCTGCCCCACAGATATACACATGTGTATAGCTGTGAGGGGACATGT	1260
Db	1205	TGCTGTACACACACAGACATCTGTGCCCTTCAAGGGCTTCAATATGTGTGTGTGTGTGTGTGT	1264
QY	1261	CACCGAGAGGACGATATCGTGTGTGACTGTGAGTGTGAGAAATGTCTGGCGCGCGGTGTCTTA	1320

```

Db 1265 CAGAAAGGAGACATGGTGGCTGGCCGAGAGAGATACCTGCCCGCAGACMACCCCG 1324
Oy 1321 TCCCAACCCAGAGATGGCTGTGACACAGACACAGCTGCCCGGAGGAACTTCG 1380
Db 1325 CTCCTAATTTGGAGATATCGGTGTGACACAGCATACCAAGTGGCCAGTAGGCAAACTTC 1384
Oy 1381 TCCCGGAGCAGAGGTGGAGCTGGGGCTGCTGCCAGTTGCCCATGCTGTGTCTCGAG 1440
Db 1385 TCCCGGAGCAGAGGTGGAGCTGGGGCTGCTGCCAGTTGCCCATGCTGTGTCTCGAG 1444
Oy 1441 GATCGCCAGCATCTGCTGCCCGGCTGCTACACCTGACAGGTGAAGCTGTGATCTCGAG 1500
Db 1445 GACCGGAGCAGAGGTGGAGCTGGGGCTGCTGCCAGTTGCCCATGCTGTGTCTCGAG 1504
Oy 1501 AAGGAGAGTGTCTGCGCCAGCTGCCAGCTTGGCCGAGTGGCCGAGCTGAGGCTGAG 1560
Db 1505 AAGGAGAGTGTCTGCGCCAGCTGCCAGCTTGGCCGAGTGGCCGAGCTGAGGCTGAG 1560
Oy 1561 AAGGAGAGTGTCTGCGCCAGCTGCCAGCTTGGCCGAGTGGCCGAGCTGAGGCTGAG 1620
Db 1561 --GAATGTGAGTGTGAGAGAGGAGCATTTCTGCATGATACAGACCTGTTGAAAGAC 1618
Oy 1621 AACCGACAGGCTGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Db 1619 AGTGCAGAGTGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1678
Oy 1681 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Db 1679 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1738
Oy 1741 GCCCGGCTGGGAGCCCTTTGAGAGGACCCAGCTTGGAGACAGCTGCTGAGAGGACA 1800
Db 1739 ATTCTGCTGGGAGATGTTTGGAGGAGTCCGCTGCCAAGCCCTACTGTAAGGAAG 1798
Oy 1801 GATACGAA-----GACTGTGACGCCCTGGGAGCCGCTGAGAGGCTGCTGCTGCTG 1853
Db 1799 GCTACAGACTTAAAGAACTCCACAGCTCGGAGACCTGTTCCGAGGAGTACCACTAC 1858
Oy 1854 AGGCTTCCCTAGACACCTCCCTTAACCAAAATTTCTCCCTGAGACCCCAATTTCTAG-CTCC 1912
Db 1859 AGGCTTCCCTAGACACCTCCCTTAACCAAAATTTCTCCCTGAGACCCCAATTTCTAG-CTCC 1918
Oy 1913 ATCACCATTGGAGGTGGGCTGCTAACTTAAGGCTTCCCTGCTGACAGAGGAGGTTGAG- 1971
Db 1919 ATCACCATTGGAGGTGGGCTGCTAACTTAAGGCTTCCCTGCTGACAGAGGAGGTTGAG- 1978
Oy 1972 CAAAGGCCATTACAAAGTGCATCCCTCCGCTTTCAGTGGAGCCCTGAGCCAGGTGC 2031
Db 1979 CAAAGGCCATTACAAAGTGCATCCCTCCGCTTTCAGTGGAGCCCTGAGCCAGGTGC 2038
Oy 2032 TTTTCCCTATCCACAGGGGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2069
Db 2039 TCTTCCCGAGCCAGAGGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2076

```

RESULT 15

MEPRT1 2100 bp mRNA linear ROD 26-AUG-1992

LOCUS M.musculus mRNA for epithelin 1 and 2.

DEFINITION X62321

ACCESSION X62321.1 GI:50851

VERSION

KEYWORDS epithelial cell growth regulator; Epithelin 1; Epithelin 2; soluble protein.

SOURCE Mus musculus.

ORGANISM Mus musculus.

REFERENCE 1 (bases 1 to 2100)

AUTHORS Plozman,G.D., Green,J.M., Neubauer,M.G., Buckley,S.D., McDonald,V.L., Todaro,G.J. and Shoyab,M.

TITLE The epithelin precursor encodes two proteins with opposing activities on epithelial cell growth

```

JOURNAL J. Biol. Chem. 267 (18), 13073-13078 (1992)
MEDLINE 92317004
PUBMED 161805
REFERENCE 2 (bases 1 to 2100)
AUTHORS Plozman,G.D.
TITLE Direct Submission
JOURNAL Submitted (15-JAN-1991) G.D. Plozman, Oncogen, 3005 1st Avenue, Seattle, WA 98121, U S A
COMMENT X62320-2.
FEATURES
    source
        1..2100
            /organism="Mus musculus"
            /db_xref="taxon:10090"
            /cell_line="kidney T cell genomic"
            /tissue_type="kidney"
            /clone_idb="lambda fixIII, PCR clones in Bluescript"
            8..1777
                /codon_start=1
                /product="Epithelin 1 & 2"
                /protein_id="CAA44197.1"
                /db_xref="GI:50852"
                /db_xref="MGD:MG1:95832"
                /db_xref="SWISS-PROT:P28798"
                /translation="MWVILMSWLAPAGLVACTGCPDQPCFVACCLIDGGANSCNP
                LLDWPRITSHHLDGSCQTHGCHPAGVSLTLTVSTSCCPFSKGVSCGDBYHCCPDG
                FHCADGKSCFQMSDNPGLGAVQCDSQFECPSATCCIMVDSWGCPPMOASCEDE
                VHCCPHGASCDLVHTRGVSPGTGTHLKKPAOKTNNAVSLPFSVCPDPAKTCPPDS
                TCCELPKGVKSCVCPGPNPNAICSDHLHCCPDPTGVDLIOSKCLSNVTTDLITKRGYP
                VKEVKCKMEVSCSPRGYTCRINTAMGCCPPAKAVCCEDHHCRCRPAFOCHTEKTE
                MGIIQVPMKRVIVAPRLPDQILKSDPDCDFRCPTNNKCKLNSGDWCCPTIPA
                VCCSDNHCPCPGFTCLAQGYCQKGDVMALEKIPARQTPDIDIGIDQHTSCPV
                GQTCPSLKGSMACCOLPNAVCCEDRHCPCAGYTCNVKARTCEKDVDFIOPVLLTL
                GPKNVNEGSGHFCNDNQCXDSAGVMACCPYLKGVCCBDRHCCPGFHCASRG
                KLRKKIIPRMWFLRDPVRL"
                8..58
                    sig_peptide
                    mat_peptide
                    59..1774
                        /product="Epithelin 1 & 2"
                        119..121
                            misc_feature
                            /note="pot. glycosylation site"
                            182..349
                                misc_feature
                                /note="pot. glycosylation site"
                                374..544
                                    misc_feature
                                    /note="cysteine-motif 1"
                                    620..790
                                        misc_feature
                                        /note="cysteine-motif 2"
                                        845..1012
                                            misc_feature
                                            /note="Epithelin 2"
                                            1091..1255
                                                misc_feature
                                                /note="Epithelin 1"
                                                1124..1126
                                                    misc_feature
                                                    /note="cysteine-motif 5"
                                                    /note="pot. glycosylation site"
                                                    1325..1492
                                                        misc_feature
                                                        /note="cysteine-motif 6"
                                                        1550..1717
                                                            misc_feature
                                                            /note="cysteine-motif 7"
                                                            1583..1585
                                                                misc_feature
                                                                /note="pot. glycosylation site"
                                                                BASE COUNT 430 a 602 c 571 g 497 t
                                                                ORIGIN
Query Match 57.2%; Score 1198.2; DB 10; Length 2100;
Best Local Similarity 75.7%; Pred. No. 7.1e-252;
Matches 1569; Conservative 0; Mismatches 483; Indels 21; Gaps 6;

```

Oy 6 GCAGACATGTGGACCCGCTGAGTGGCTGCTTACACAGAGGCTGCTGGAGAC 65

Db 1 GCAGACATGTGGCTGCTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60

Oy 66 GCGGTGCCAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 125

Db 61 ACAGTGTCCAGATGTGGGACAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120

Oy 126 CTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 185

```

1195 AGACAACAGAGATTCCTCCCTCAGGGCTTACATGTCGTCTCAGGGTACTGTACAGAA 1254
1266 AGGAGCAGATCTGTGGCTGACACTGAGAGATGCTGCGCGCGGTCTCTTATCCCA 1325
1255 GGGAGACAAATGTGTGGCTGCGCTGAGAGATACCTCCGCGAGAACACCCGCTCCA 1314
1326 CCCAGACATGGGTGTGACACAGACACAGCTGCGCGGTGGCGGAGAACCTGTGCC 1385
1315 AATTGAGATATGCTGTGTGACACAGATACCTGCGCGAGTAGGGCAACCTGTGCC 1374
1386 GAGCAGAGGTGGAGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1434
1375 AAGCTCAAGAGAGATGGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1505
1446 CAGACATGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1494
1435 GCAGCATGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1565
1506 AGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1548
1495 TGTGATTTATCCAGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1625
1566 CAGGAGTGTGGGAGAGACATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1608
1549 TGTGAGTGTGGAGAGAGAGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1685
1626 ACAGGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1668
1609 AGGATGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1745
1686 CAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1728
1669 TTGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1805
1746 GCGTGGGAGCGCTTGTAGGAGACCCAGCTGAGAGAGCTGCTGAGGACATGCT 1788
1729 TCGTGGGAGATTTTGTAGGAGATCGGCTGAGAGACCGCTGCTGAGAGAGGCT 1858
1806 GAA-----GACTCTGACGCTCTGAGACCCAGCTGAGAGAGGCTGCTGCTGCT 1848
1789 AGACTTAAAGAGATCCAGATCTGAGAGACCGCTGAGAGAGGCTGCTGCTGCTG 1917
1859 TCCCTAGGACCTCCCTTAAACCAATTCCTGAGAGAGGCTGCTGCTGCTGCTGCT 1908
1849 TCCCTAGGACCTCCCTTAAACCAATTCCTGAGAGAGGCTGCTGCTGCTGCTG 1976
1918 CATGAGAGGTGGGCTCATATCTAAGGCTTCCCTGAGAGAGGCTGCTGCTGCT 1968
1909 CATTAAGGTGGGCTCAAACTAAACCTTCTTATGAGAGAGGCTGCTGCTGCT 2036
1977 GCCATTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2028
1969 GCCCGTATCAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2069
2037 CCTATCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2061
2029 CCGAGCCACAGGTGCTGAGAGCTTGTG 2061

```

Search completed: February 21, 2003, 14:34:59
 Job time : 5408 secs

THIS PAGE BLANK 103

D	b	121	GCACAGCTACAGACTGTCTGCGCGCCCTTCGTGGACAATAATGGCCACACACTGAGCAGGCAT	180
Q	y	181	CTGGGTGGCCCCCTCCAGAGTTGATGCCACTGCTCTGCGGGCCACTCTGTGCATCTTTTACC	240
D	b	181	CTGGGTGGCCCCCTCCAGAGTTGATGGCCCACTGCTCTGCGGGCCACTCTGTGCATCTTTTACC	240
Q	y	241	GTCACAGGACTTTCATATGCTGCGCCCTTCCAGAGCCGTGGCAATGGGGGATGGCCAT	300
D	b	241	GTCACAGGACTTTCATATGCTGCGCCCTTCCAGAGCCGTGGCAATGGGGGATGGCCAT	300
Q	y	301	CACGTCTGCCACAGGGGCTTCCACTGTCAGTGCAGAGGGGAGTCCGTCTTCCAAAGATCA	360
D	b	301	CACGTCTGCCACAGGGGCTTCCACTGTCAGTGCAGAGGGGAGTCCGTCTTCCAAAGATCA	360
Q	y	361	GGTAACTCCTCGTGGGTGCCATCCATGCCCTGATATGATCGAATGCCAGGCCGACTTC	420
D	b	361	GGTAACTCCTCGTGGGTGCCATCCATGCCCTGATATGATCGAATGCCAGGCCGACTTC	420
Q	y	421	TCACAGTCTGTATTATGTGCGATGGGTCTCTGGGGGGTGGCCCATATGGCCCAAGCTTC	480
D	b	421	TCACAGTCTGTATTATGTGCGATGGGTCTCTGGGGGGTGGCCCATATGGCCCAAGCTTC	480
Q	y	481	TGCTGTGAAGACAGAGGTGCATGCTGTCTCCACAGGTGCCTTTCGCACACTGGTTCACAC	540
D	b	481	TGCTGTGAAGACAGAGGTGCATGCTGTCTCCACAGGTGCCTTTCGCACACTGGTTCACAC	540
Q	y	541	CGCTGCATCACACCACAGGGCACCCCTCTGGCAAGATGCTCCCTGCCACAGAGACT	600
D	b	541	CGCTGCATCACACCACAGGGCACCCCTCTGGCAAGATGCTCCCTGCCACAGAGACT	600
Q	y	601	AACAGGGCAGTGGCTTGTCCAGTGTGGTATGTGTCCGAGCACAGTCCGGTGGCCCT	660
D	b	601	AACAGGGCAGTGGCTTGTCCAGTGTGGTATGTGTCCGAGCACAGTCCGGTGGCCCT	660
Q	y	661	GATGGTTCTACCTCTGTGAGCTGCCAGTGGGAAATATGGTGTGTCGCCAATGCCCAAC	720
D	b	661	GATGGTTCTACCTCTGTGAGCTGCCAGTGGGAAATATGGTGTGTCGCCAATGCCCAAC	720
Q	y	721	GCCACCTGCTCTCCGATCACCTGCATGCTGCCCCCAAGACACTGTGTGTGACTGTATC	780
D	b	721	GCCACCTGCTCTCCGATCACCTGCATGCTGCCCCCAAGACACTGTGTGTGACTGTATC	780
Q	y	781	CAGAGTAGTGCCTCTCCAAAGGAAAGCTACACAGGACTCTCTCAATAGCTGCTGGG	840
D	b	781	CAGAGTAGTGCCTCTCCAAAGGAAAGCTACACAGGACTCTCTCAATAGCTGCTGGG	840
Q	y	841	CACACAGTGGCGATGTGAATGTGACATGAGGTGAGTGCCTCCCAATAGCTATACCTGC	900
D	b	841	CACACAGTGGCGATGTGAATGTGACATGAGGTGAGTGCCTCCCAATAGCTATACCTGC	900
Q	y	901	TGCGCTTCACTAGTGGGGGCTGGGGCTGCTGCCCTTTTACCAGGCTGTGTCTGTAG	960
D	b	901	TGCGCTTCACTAGTGGGGGCTGGGGCTGCTGCCCTTTTACCAGGCTGTGTCTGTAG	960
Q	y	961	GACCACATACCTGCTGTCCCGGGGGTTTACGTGACACGCAAGAAAGGTACTGTGAA	1020
D	b	961	GACCACATACCTGCTGTCCCGGGGGTTTACGTGACACGCAAGAAAGGTACTGTGAA	1020
Q	y	1021	CAGGGGCCCCCAGAGTGCCTTGATGGAAGAGGCCCAAGCTCAGCTGCGCAGAC	1080
D	b	1021	CAGGGGCCCCCAGAGTGCCTTGATGGAAGAGGCCCAAGCTCAGCTGCGCAGAC	1080
Q	y	1081	CCACAAGCTTTGAAGAGATGTCCCTGTGATTAATGTACAGAGCTGTCCCTCTCCGAT	1140
D	b	1081	CCACAAGCTTTGAAGAGATGTCCCTGTGATTAATGTACAGAGCTGTCCCTCTCCGAT	1140
Q	y	1141	ACCTGTGCCCAATCAGTCTGGGGAGTGGGGCTGCTGTTCATCTCCCAAGGCTGTCTGC	1200
D	b	1141	ACCTGTGCCCAATCAGTCTGGGGAGTGGGGCTGCTGTTCATCTCCCAAGGCTGTCTGC	1200
Q	y	1201	TGCTGTGGACACAGCACTGTGCCCGCCACAGATACAGTGTACTGTAGGGGCGAGTGT	1260
D	b	1201	TGCTGTGGACACAGCACTGTGTGCCCGCCACAGATACAGTGTACTGTAGGGGCGAGTGT	1260

QY	1261	CAGGAGGAAACGAGATCGTGGGCTGGAGCTGGAAATATGCTCTGGCCGCGGGGTTCTTAA	1320
Db	1261	CAGGAGGAAACGAGATCGTGGGCTGGAGCTGGAAATATGCTCTGGCCGCGGGGTTCTTAA	1320
QY	1321	TCCACACCCAGAGATCGGCTGTGACACACACACACAGCTGCCGGTGGGCGAAACCTGC	1380
Db	1321	TCCACACCCAGAGATCGGCTGTGACACACACACACAGCTGCCGGTGGGCGAAACCTGC	1380
QY	1381	TGCCGAGCCAGGGTGGGAGCTGGGCTGTGCTGCCAGTTGGCCCATATCTGTGTGTCCGAG	1440
Db	1381	TGCCGAGCCAGGGTGGGAGCTGGGCTGTGCTGCCAGTTGGCCCATATCTGTGTGTCCGAG	1440
QY	1441	GATGCACGACACTCTCCGCGGCTGAGCTACCTGGCAAGCTGAAAGGCTGATCTCTGCGAG	1500
Db	1441	GATGCACGACACTCTCCGCGGCTGAGCTACCTGGCAAGCTGAAAGGCTGATCTCTGCGAG	1500
QY	1501	AAGGAAGTGTCTGTGCCACAGCCTGCACACTTCTGGCCCGTAGCCCTACGCTGGGTGTG	1560
Db	1501	AAGGAAGTGTCTGTGCCACAGCCTGCACACTTCTGGCCCGTAGCCCTACGCTGGGTGTG	1560
QY	1561	AAGGACGTGGAGTGTGGGGGAAAGACACTTGTGGCAATGATTAACACAGCTGTCTGCCGAGAC	1620
Db	1561	AAGGACGTGGAGTGTGGGGGAAAGACACTTGTGGCAATGATTAACACAGCTGTCTGCCGAGAC	1620
QY	1621	AACGACAGGGCTGGGCTCTGCTGCCCTACAGCCACAGGCGTGTGTGTCTATCTAGCGGC	1680
Db	1621	AACGACAGGGCTGGGCTCTGCTGCCCTACAGCCACAGGCGTGTGTGTCTATCTAGCGGC	1680
QY	1681	CACTGTCTGTCTGTGGCTTCCTCCGCTGCGACGACGAGGGATACCAAGTGTGTGCGCAGGGAG	1740
Db	1681	CACTGTCTGTCTGTGGCTTCCTCCGCTGCGACGACGAGGGATACCAAGTGTGTGCGCAGGGAG	1740
QY	1741	GCCCCGGCTGGGACGCCCCCTTTGAGGAGACACGACCTTGAGACAGCTGTGTGAGGAGACA	1800
Db	1741	GCCCCGGCTGGGACGCCCCCTTTGAGGAGACACGACCTTGAGACAGCTGTGTGAGGAGACA	1800
QY	1801	GTACTGAAGACTCTGACAGCCCTCGGGACCCCACTCGGAGAGGTGCCCCCTGTCAAGGCTTC	1860
Db	1801	GTACTGAAGACTCTGACAGCCCTCGGGACCCCACTCGGAGAGGTGCCCCCTGTCAAGGCTTC	1860
QY	1861	CCTAGCACTCTCCCTTAACCAAAATTCCTCCGTGAGACCCCATTTCTAGACTTCCCATACCAT	1920
Db	1861	CCTAGCACTCTCCCTTAACCAAAATTCCTCCGTGAGACCCCATTTCTAGACTTCCCATACCAT	1920
QY	1921	GGGAGGTGGGGCTCATCTTAAGGCCCCCTTCCCTGTGAGAAAGGGGGTTGAGGGCAAAAGCC	1980
Db	1921	GGGAGGTGGGGCTCATCTTAAGGCCCCCTTCCCTGTGAGAAAGGGGGTTGAGGGCAAAAGCC	1980
QY	1981	ATTACAACTGTCATCCCTCCCTCCCGTTTCAGTGGACCTGTGTGGCCAGGTGCTTTTCCCTA	2040
Db	1981	ATTACAACTGTCATCCCTCCCTCCCGTTTCAGTGGACCTGTGTGGCCAGGTGCTTTTCCCTA	2040
QY	2041	TCCACAGGGGCTTGTGTGTGTGTGGGTGTGCTTTCATTAAGTTTGTCACTTTCTT	2095
Db	2041	TCCACAGGGGCTTGTGTGTGTGTGGGTGTGCTTTCATTAAGTTTGTCACTTTCTT	2095
RESULT 2			
US-09-813-156-16			
Sequence 16, Application US/09813156			
Patent No. US20020061859A1			
GENERAL INFORMATION:			
APPLICANT: Serreio, Ginette			
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTIACONISTS			
FILE REFERENCE: 2996.488/P001-A			
CURRENT APPLICATION NUMBER: US/09/813,156			
PRIOR FILING DATE: 2001-03-21			
PRIOR APPLICATION NUMBER: 08/991,862			
PRIOR FILING DATE: 1997-12-16			
PRIOR APPLICATION NUMBER: 08/863,862			
PRIOR FILING DATE: 1997-05-23			
NUMBER OF SEQ ID NOS: 17			

|||||
Db 1921 GGGAGGTGGGCTCAATCTTAAGGCCCTTCCTGTCAGAGAGGGGGTGGAGAAAAGCCC 1980
Oy 1981 ATTACAGCTGCATCCCTCCCGTTTCAGTGAAGCCGTGGCCAGAGGCTTTTCCCTA 2040
Db 1981 ATTACAGCTGCATCCCTCCCGTTTCAGTGAAGCCGTGGCCAGAGGCTTTTCCCTA 2040
Oy 2041 TCCACAGGGGGTGTGTGTGTGGGTGTGCTTTCAATAAAGTTTGTACATTCTT 2095
Db 2041 TCCACAGGGGGTGTGTGTGTGGGTGTGCTTTCAATAAAGTTTGTACATTCTT 2095

RESULT 3

US-09-824-807-16
: Sequence 16, Application US/09824807
: Patent No. US20020094966A1
: GENERAL INFORMATION:
: APPLICANT: Serrero, GINETTE
: TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
: FILE REFERENCE: 2996.488/P001-A
: CURRENT APPLICATION NUMBER: US/09/824.807
: PRIOR FILING DATE: 2001-04-04
: PRIOR APPLICATION NUMBER: 08/991,862
: PRIOR FILING DATE: 1997-12-16
: PRIOR APPLICATION NUMBER: 08/863,862
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 16
: LENGTH: 2095
: TYPE: DNA
: ORGANISM: Human GP88 CDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (13)..(1791)
: OTHER INFORMATION: Nucleotide sequence of human granuln/epithelin
: OTHER INFORMATION: precursor (human GP88). Human Granulin Genebank
: OTHER INFORMATION: M75161.
US-09-824-807-16

Query Match 100.0%; Score 2095; DB 10; Length 2095;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2095; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGCAGGAGAGACCATGTGACCCCTGTGAGCTGGTGGCCCTTAACAGCAGGGGTGTGGCT 60
Db 1 CGCAGGAGAGACCATGTGACCCCTGTGAGCTGGTGGCCCTTAACAGCAGGGGTGTGGCT 60
Oy 61 GGAAGCGCGTGGCCAGATGTGATGTTCTGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG 120
Db 61 GGAAGCGCGTGGCCAGATGTGATGTTCTGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG 120
Oy 121 GGCAGCTACAGTGTGCTGCTCCCTTTCGACAAATGAGCCCAACAACATGAGCAGCAT 180
Db 121 GGCAGCTACAGTGTGCTGCTCCCTTTCGACAAATGAGCCCAACAACATGAGCAGCAT 180
Oy 181 CTGGGTGGCCCTCGCAGAGTTGATGCCACTGCTGTGCCGCGCACCTCTGCATCTTTACC 240
Db 181 CTGGGTGGCCCTCGCAGAGTTGATGCCACTGCTGTGCCGCGCACCTCTGCATCTTTACC 240
Oy 241 GTCCTAGGAGACTTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 241 GTCCTAGGAGACTTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Oy 301 CACTGTGCTGCCAGGGGCTTCCACTGACAGTGCAGAGGGGCGATCTGCTTCCAAAGATCA 360
Db 301 CACTGTGCTGCCAGGGGCTTCCACTGACAGTGCAGAGGGGCGATCTGCTTCCAAAGATCA 360
Oy 361 GGTAAACAATCTCGTGGGTGCATTCAGTGCCTGATAGTACATGATGATGATGATGATGATG 420
Db 361 GGTAAACAATCTCGTGGGTGCATTCAGTGCCTGATAGTACATGATGATGATGATGATGATG 420
Oy 421 TCCACGTCTGTATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480

|||||
Db 421 TCCACGTCTGTATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
Oy 481 TCGTGTGAAGAGAGAGGTGACAGTGTGTCGCGACGGGCGCTTTCGACATGATGATGATG 540
Db 481 TCGTGTGAAGAGAGAGGTGACAGTGTGTCGCGACGGGCGCTTTCGACATGATGATGATG 540
Oy 541 CGCTGCATCACACCCAGGGGCAACCCCTTGGCAAGAGTCTCCCTCCAGAGAGACT 600
Db 541 CGCTGCATCACACCCAGGGGCAACCCCTTGGCAAGAGTCTCCCTCCAGAGAGACT 600
Oy 601 AACAGGGAGTGGCTTGTTCAGCTGTGATGTGTGTCGAGCGACAGGTCGCCGTGCTT 660
Db 601 AACAGGGAGTGGCTTGTTCAGCTGTGATGTGTGTCGAGCGACAGGTCGCCGTGCTT 660
Oy 661 GATGTTCTACCTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
Db 661 GATGTTCTACCTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
Oy 721 GGCACCTGCTGCTCCGATCAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 721 GGCACCTGCTGCTCCGATCAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Oy 781 CAGAGTAAGTGCCTTCCAAAGGAAGCCTTACCAGGACCTCTCACTAAGCTGCTGCG 840
Db 781 CAGAGTAAGTGCCTTCCAAAGGAAGCCTTACCAGGACCTCTCACTAAGCTGCTGCG 840
Oy 841 CACACAGTGGGGATGTAATGTGATGATGATGATGATGATGATGATGATGATGATGATG 900
Db 841 CACACAGTGGGGATGTAATGTGATGATGATGATGATGATGATGATGATGATGATGATG 900
Oy 901 TCCGCTCTACAGTGGGGGCTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 901 TCCGCTCTACAGTGGGGGCTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Oy 961 GACCAATACATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db 961 GACCAATACATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Oy 1021 CAGGGGCCCCACAGAGTGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Db 1021 CAGGGGCCCCACAGAGTGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Oy 1081 CCACAAGCCTTGAAGAGATGTCCCTGTGATGATGATGATGATGATGATGATGATGATGAT 1140
Db 1081 CCACAAGCCTTGAAGAGATGTCCCTGTGATGATGATGATGATGATGATGATGATGATGAT 1140
Oy 1141 ACCTGTGCTCAACTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Db 1141 ACCTGTGCTCAACTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Oy 1201 TCGTGGAGACACAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
Db 1201 TCGTGGAGACACAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
Oy 1261 CAGCGAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
Db 1261 CAGCGAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
Oy 1321 TCCCAACCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
Db 1321 TCCCAACCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
Oy 1381 TCCCGAGGAGAGTGGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
Db 1381 TCCCGAGGAGAGTGGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
Oy 1441 GATCGCAGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
Db 1441 GATCGCAGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
Oy 1501 AAGGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560

Db 1501 AAGGAAGTGTCTTCCGACGCTGCGACCTTCTGCGCCCGTACGCTTACGTTGGTGTG 1560
QY 1561 AAGGAGCTGAGTGTGGGAGAGACACTTCTGCAATGATTAACGACACTGTGTCCGAGAC 1620
Db 1561 AAGGAGCTGAGTGTGGGAGAGACACTTCTGCAATGATTAACGACACTGTGTCCGAGAC 1620
QY 1621 AACCCAGAGGCTGGGCTGTGTCTTACGCCAGGCGGTCTGTGTGTGTATGCGCGC 1680
Db 1621 AACCCAGAGGCTGGGCTGTGTCTTACGCCAGGCGGTCTGTGTGTGTATGCGCGC 1680
QY 1681 CACTGTGTCTGT 1740
Db 1681 CACTGTGTCTGT 1740
QY 1741 GCCCGGCTGGGAGCGCCCTTTGAGGAGCCAGCCTTGAAGAGCTGTGTGTGTGTGTGTGT 1800
Db 1741 GCCCGGCTGGGAGCGCCCTTTGAGGAGCCAGCCTTGAAGAGCTGTGTGTGTGTGTGTGT 1800
QY 1801 GTACTGAAACTCTGTGACGCTGTGAGACCCACTGAGAGGTCCTGTGTGTGTGTGTGTGT 1860
Db 1801 GTACTGAAACTCTGTGACGCTGTGAGACCCACTGAGAGGTCCTGTGTGTGTGTGTGTGT 1860
QY 1861 CTTAGACCTTCCCTTAACCAATCTCTGCTGAGACCCCAATCTGAGCTCCCAATCAACCAAT 1920
Db 1861 CTTAGACCTTCCCTTAACCAATCTCTGCTGAGACCCCAATCTGAGCTCCCAATCAACCAAT 1920
QY 1921 GGGAGGTGGGCGCTCAATCTAAGGCGCTTCCCTGTGAGAGAGGCGGTGAGCAAAAGCCC 1980
Db 1921 GGGAGGTGGGCGCTCAATCTAAGGCGCTTCCCTGTGAGAGAGGCGGTGAGCAAAAGCCC 1980
QY 1981 ATTACAGCTGCTATCCCTCCCTGTTTCAATGTGAGACCTGTGTGTGTGTGTGTGTGTGT 2040
Db 1981 ATTACAGCTGCTATCCCTCCCTGTTTCAATGTGAGACCTGTGTGTGTGTGTGTGTGTGT 2040
QY 2041 TCCACAGGCGGT 2095
Db 2041 TCCACAGGCGGT 2095

RESULT 4

US-09-925-301-574

Sequence 574, Application US/09925301

Patent No. US20020052308A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925,301

PRIOR APPLICATION NUMBER: PCT/US00/05882

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 574

LENGTH: 2432

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (7)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc_feature

LOCATION: (2326)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc_feature

LOCATION: (2367)

OTHER INFORMATION: n equals a,t,g, or c

US-09-925-301-574

Query Match 96.1%; Score 2014; DB 10; Length 2432;
Best Local Similarity 99.2%; Pred. No. 0;

Matches 2045; Conservative 0; Mismatches 15; Indels 2; Gaps 2;
QY 1 CGCAGCGAGACATGTGAGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 60
Db 176 CGCAGCGAGACATGTGAGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 235
QY 61 GGAACGCGGTGCCAGATGTCAGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
Db 236 GGAACGCGGTGCCAGATGTCAGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 295
QY 121 GCCAGTACAGTCGT 180
Db 296 GCCAGTACAGTCGT 355
QY 181 CTGGGTGGCCCTGCCAGGT 240
Db 356 CTGGGTGGCCCTGCCAGGT 415
QY 241 GTCTCAGGGACTTCCAGTTGT 300
Db 416 GTCTCAGGGACTTCCAGTTGT 475
QY 301 CACTGT 360
Db 476 CACTGT 535
QY 361 GGTAAACACTCGT 420
Db 536 GGTAAACACTCGT 595
QY 421 TCCAGT 480
Db 596 TCCAGT 655
QY 481 TGTGTGAAGACAGGGGTGCTGT 540
Db 656 TGTGTGAAGACAGGGGTGCTGT 715
QY 541 CGCTGCATCACACCAACGAGGACCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
Db 716 CGCTGCATCACACCAACGAGGACCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 775
QY 601 AACAGGGCACTGT 660
Db 776 AACAGGGCACTGT 835
QY 661 GATGTGTCTACGTCGT 720
Db 836 GATGTGTCTACGTCGT 895
QY 721 GCCACGT 780
Db 896 GCCACGT 955
QY 781 CAGAGTAAGT 840
Db 956 CAGAGTAAGT 1015
QY 841 CACACAGTGGCGATGGAATGTGACATGAGTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Db 1016 CACACAGTGGCGATGGAATGTGACATGAGTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1075
QY 901 TGCCTGTCTACAGT 960
Db 1076 TGCCTGTCTACAGT 1135
QY 961 GACCAATATACATGT 1020
Db 1136 GACCAATATACATGT 1195
QY 1021 CAGGGGCCCCAGAGGT 1080
Db 1196 CAGGGGCCCCAGAGGT 1255

[illegible]

```

1  Publication NO. US20020183270A1
2  GENERAL INFORMATION:
3  APPLICANT: Serrero, GINETTE
4  TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
5  FILE REFERENCE: Z9996,488/P001-A
6  CURRENT APPLICATION NUMBER: US/09/824,647
7  CURRENT FILING DATE: 2001-04-04
8  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862
9  PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17
10 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/863,862
11 PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
12 NUMBER OF SEQ ID NOS: 17
13 SOFTWARE: PatentIn Ver. 2.0
14 SEQ ID NO 1
15     LENGTH: 2137
16     TYPE: DNA
17     ORGANISM: Mouse epithelin/granulin
18     FEATURE:
19     NAME/KEY: CDS
20     LOCATION: (23)..(1789)
21     OTHER INFORMATION: The sequence is identical to that of the published
22     OTHER INFORMATION: mouse granuln except for one nucleotide (T
23     OTHER INFORMATION: instead of G) at position 1071 of GP88 CDNA
24     OTHER INFORMATION: (position 1056 of mouse granuln).
25 OS-09-824-647-1

```

Query Match	57.3%	Score 1200; DB 9;	Length 2137;
Best Local Similarity	75.6%	Pred. No. 8e-315;	
Matches 1572; Conservative	0;	Mismatches 485;	Indels 21; Gaps 6

[illegible]

RESULT 5
US-09-824-647-1
; Sequence 1, Application US/09824647

QY	1	CGCAGGACGACATGTGGACCCCTGGTAGCGGGGTGCCTTAAACAGCAGGGCTGTGGCT	60
Db	11	CGCAGACGACGACATGTGGGTCTTATAGCTGGCTGGCTTCCGGCAGGGGCTGTAGCC	70
QY	61	GGAACGGGTGCCAGATGGTCACTTGCCTGTGTGGCTGTGCATGGACCCGGAGGA	120
Db	71	GGAACAGAGTGTCCAGATGGGCACTTGTGGCTGTGGTCCGTGGCTTGAACAGGGAGGA	130
QY	121	GCCAGCTACAGCTCTGTGCGGTCCTTGTGGACAAATGGGCCAACACAGACAGGCAT	180
Db	131	GCCAACTACAGCTCTGTAAACCTCTTCTTGGACATAGGCGCTTGAATATACAGGCATCAT	190
QY	181	CTGGGTGGCCCCCTGCCAGAGTTGATGCCACTGTCTCTGCTCGGCCACTCTGCATCTTTACC	240
Db	191	CTAATGTGCTCTCTGCAGACCATGGCCACTGTCTCTGTGGCATTTCTTGTCTTCACT	250
QY	241	GTCACAGGACATTCAGTTGTGTGCCCCCTTCCACAGGCCCTGGCATGCGGGGATGGCAT	300
Db	251	GTGTCTGGACATTCACACTGTGTGCCCTTCTCTAAAGGTTGTCTTGTGTGTGATGGCTAC	310
QY	301	CACGTGTGCCACAGGGGCTTCCATGTGAGTAGACAGCGGGGATGCTCTTCCAAAGATCA	360
Db	311	CACGTGTGCCCCAGGGCTTCCATGTGATAGTAGACATGGAAATCTGTCTCCAGATGTCA	370
QY	361	GGTAAACATCTCGTGGTGGCCATCCAGTGGCCTGTAGTAGTCAGTTGCAATGCCGGACTTC	420
Db	371	G---ATAACCCCTTGGGTGTGTCTCAATGTCTCTGGAGCCAGTTGTAATCTCTGACTCT	427
QY	421	TCCAGGTGTGTATTATGTGTGATAGGTGCTCTGGGGGGTGTGCCCATAGCCCCAGGCTTC	480
Db	428	GCCACCTGTCTCAATTATGTGTGAATGGTGTGGGGGATGTGTCTCCATAGCCCCAGGCTCT	487
QY	481	TGCTGTGAAGACAGAGGTGCATGCTGTGCCGACAGGTGCTTGTGCGACTGTGTACACC	540
Db	488	TGCTGTGAAGACAGAGTGCATGTGTGTGCCCATGGGGCTCTGTGTGACTGTGTTCACACA	547
QY	541	CGGTGCATCACCCACGCGGACCCACCCCTGGCAAAGAGCTCCCTGGCCAGAGACT	600
Db	548	CGATGCGTTTACCCACAGGGGACCCACACCTACTATAAGAAAGTTCCCTGCACAAAAGACC	607
QY	601	AACAGGGCAGTGGCTGTGCAGTGTGGTCAATGTGTCCGAGACGACAGTCCCGGTGCTT	660
Db	608	AACAGCGCAGTGTCTTGGCTCTTTTCTGTGTGTGGCTTATGTCTTAAGACCAAGTGTCCC	667

OY	241	GTCACAGGACTTCCACATGTGGTGCCCCCTTCCACAGAGGCCGTGGCAATCGSGGGATATGGCAT	300
Db	251	GTGTCTGGGACTTCCACAGTGTGCCTCCCTTTCTTAAGGCTGTGTCTGTGTATGGCTAC	310
OY	301	CACGTCTGCCACCACGGGGCTTCCATGTGCAGTGCAGACGGGCGATCCGTCTTCCAAGAATCA	360
Db	311	CACGTCTGCCACCACGGGGCTTCCATGTAGTAGCAGATATGGGAATCTCGTCTTCCAGATTGCA	370
OY	361	GCTAACCACTCCGTTGGGTGCCATTCAGTGTGCCCTTGATATGTCAGTTCGAATGCCGACATTC	420
Db	371	G---ATAACCCCCTGGGGTGTCTCCATGTCTCCAGGAGCGCAGATTGAAATGCTCTACACT	427
OY	421	TCCACGCTCTGTGTTATGTGTCGATGTGCTCTGGGGGTGTCGCCCATATGATCCCAAGCTTCC	480
Db	428	GCCACCTCTCTCATTTATGTGTTGATATGTCTGGGGAATGTTTCCATATGCCCCACAGGCTCT	487
OY	481	TGCTGTGAAGACAGAGGTGCACACTGCTGTCCGACAGGTGCCCTTCTGCGACCTGGTTCACAC	540
Db	488	TGCTGTGAAGACAAGTGCATATTCCTGTCCCAATGGGGGCTCCGCTGATCCTGTGTACACA	547
OY	541	CGCTGCATCACACCACGGGGCACCCACCCCTGGCAAABAGTCCCTTCCACAGAGACT	600
Db	548	CGATCCGTTTTACCCACAGGGGACCCACACCCCTACTAAGAAATGTCCTTCACAAAAAGAC	607
OY	601	AACAGGCAAGTGGCCCTTGTCCAGTCCGTTATGTATGTCGAGCAGCAGGTGCCGGGACCT	660
Db	608	AACACGCGAGTGTCTTGGCTTTTGTCTGTGTGTGCTCGATGTATGAACCCAGTGTCC	667
OY	661	GATGTTCTACCTCTGTGAGCTGCCACGTGGAGATATGCTGTGCCCAATGCCAAC	720
Db	668	GATGTTCTACCTCTGTGAGCTTACCCACACGGGAATATGCGTGTCTCAATGCCCAAT	727
OY	721	GCCACCTCTCTCGAATACCTGCATCGTGTGCCCCACAGACACATGTGTATACCTGATC	780
Db	728	GCCATCTGCTTTCCGACACATCTGCATGCTGTGCCCCAGACACATGTATGTACCTGATC	787
OY	781	CAGAGTAAGTGCCTTCCAAAGAGAACGCTTACACAGGACCTCTCTACTAAGCTGCCCTCG	840
Db	788	CAGAGTAAGTGCCTTATCA--AGAACTACACACAGGATCTCCTGACCAAGCTGCTCGA	844
OY	841	CACACAGTGGGCGATGTGAAATGTGACATGTGAGTGAAGCTGCCAGATGGCTATACCTGC	900
Db	845	TACCCAGTGAAGGAGGTGAATGTGGAATGTGAATGAAGTGAAGTCCCTGMAAGAAATATCTGC	904
OY	901	TGCCGTATCAGATGGGGGCGCTGGGGCTGTGTGCCCTTTTACCAGAGCTGTGTCTGTGAG	960
Db	905	TGCCGCTCAACACTGGGGGCTGGGGCTGTGTCTCATTTTGCCAAAGGCTGTGTGTGTAC	964
OY	961	GACCACTATACCTGCTGTCCCGGGGGTTTACGTGTGACACGCGAAGGGTACCTGTGAA	1020
Db	965	GATCATCTTCAATTGCTGTCCGGGCGAGGGTTTCACTGTACACAGAGAAAGAACCTGCGAA	1024
OY	1021	CAGGGGCCCCACAGGTGGCCCTGGATGGAAAAGGCCCGCACCTTCACTCAGCCTGGCAGAC	1080
Db	1025	ATGGGTATCTCCACAGTATGGGTGATGAABAAAGTATATAGCCCCCTCTCGCTGTCCAGAC	1084
OY	1081	CCACAAGCTTTGAGAGAGATGTCCCTGTGATATATGTAGACAGCTGTCCCTCTCCGAT	1140
Db	1085	CCACAAGCTTTGAGAGAGATGTGATATGATGACTTCACTAGTGTGTCTTACAAAAT	1144
OY	1141	ACCTGTGCCAATTCACGTCTGGGGATGGGGCTGTCTTCACATCCACAGAGCTGTCTGC	1200
Db	1145	ACCTGTGCCAATTCATTTCTGGGGATGGGGCTGTCTTCCATCCACAGAGCTGTCTGC	1204
OY	1201	TGCTCGGACCCACAGACACTGTGTGCCCCACAGCATTAACGTGTGTAGCTGAAGGCGACGT	1266
Db	1205	TGCTCGGACCCACAGACATGTGTGCCCTTCAAGGCTTACATGTCTGTGCTTCAAGGGTACGT	1264
OY	1261	CAGGAGGAACCGGATATCGTGGCTGTGACTGGAAATGATCGTCCCGCGCGGTTCCTTA	1320
Db	1265	CAGGAGGAACCAATGTGTGTGCTGTGGCTGTGAAATAATATCTGTCCCGGCCACAGCAACCCG	1324

OY	1321	TCCCAACCCCAGAGCATCGGCTGTGACAGCAGCACACCAGTATGCCCGGTGGGGGAACCTGC	1380
Db	1325	CTCCAAATTGGAGATATCGGTTGTGTACACAGCATTAACACTGTGCCCAAGTAGAGGCMAA	1384
OY	1381	TGCCCGAGCCAGAGGTGGAGCTGGGCTCGTCGCCAGATTGCCCAATGTGTGTGTCCGAG	1440
Db	1385	TGCCCAAGCCCTCAAGGGAAAGTAATGGGGCTCTCTGCGACAGCTCCCCCAATGTGTGTGTAG	1444
OY	1441	GATCGCAGACATGTCGCCCGGGTGCTACCTGTACCTGTGAAGTGAAGGTGATCTCGGAG	1500
Db	1445	GACCGGACGACTGTGTCCCGCGCGGGATACCTGTGAACAGTGAAGGACAGAACCTGTGAG	1504
OY	1501	AAGGAGTGTCTCTGTGCCACAGCCTGCGACACTTCCTGGGCGCCGTAGCTCAGCTGGGTGTG	1560
Db	1505	AAGATGTGCATTTTATCCAGACCTCCCGTGTCCTGTGACCTCCCTGGGCGCTAAGGTTGG	1560
OY	1561	AAGAGCTGGAGTGTGGGGAAAGAGACATTCGTGCAATGATTAACAACACTGTCTGCCAGAC	1620
Db	1561	--GAATGTGAGTGTGGAGGAAGGGACATTTCTGCAATGATTAACAACACTGTGTGTAAGAC	1618
OY	1621	AACCGAAGAGGGCTGGGCGCTCTGTCCCTACAGCCACAGGGCGTGTGTGTGATGTGCGGC	1680
Db	1619	AGTGCAGAGAGTGTGGGCGCTCTGTCTCTTCCCTACATAAAGGTGTGTGTGTGAAGATGAGCT	1678
OY	1681	CAGTGTGTCTCTGTGCTGTGCGCTTCGCGTGCACGACGAGGGGTACCAAGTGTGTGGCAGAGG	1740
Db	1679	CAGTGTGTCCCGGTGCTCTTCCACTGTTCAGCCAGGGGAACCAATGTGTTCGAAGAAG	1738
OY	1741	GCCCCGGGCTGGGAGCGCCCTTTTGAAGGAGCCAGCCTTGAGACACTGTGTGAAGGGACA	1800
Db	1739	ATTCCTGTGCTGGAGCATATGTTTTGAGAGGATCCGCTGCCAAGACCCTTACTGTGAAGAGG	1798
OY	1801	GATCTGAA-----GACTGTGAGCGCTTCGGGAGCCCACTCGAAGGGTGCCCTCTGTCTC	1853
Db	1799	GCTACAGACTTAAGGAACCTTCAACAGCTCTGGGAACCTGTTCGAGGGTACCCACTACTC	1858
OY	1854	AGGCGTCCCTAGACACCTCCCCCTTAACCAATTCCTCCCTGAGACCCATCTGTAG--CTCCCC	1912
Db	1859	AGGCGTCCCTAGAGCCCTCTGCCCCCTTAACGTCTCCCGGCTACTCATCTGTGATCACTCT	1918
OY	1913	ATCACATGGGAGGTGGGCGCTCAATCTAAGGCCCTTCCCTGTCAAGAGGGGGTGTGAG-	1971
Db	1919	ATCACATGGGAGGTGGAGCGCTCAAACTAAAACCTCTTTTATGGAAGAAAGGCTGTGGC	1978
OY	1972	CAAAAGCCCATTTACAGCTGCATCCCCCTCCCGTTAGTGTGAGACCTGTGGCCAGGTGC	2021
Db	1979	CAAAAGCCCGTATCAAACTGCCATTTCTTCGCGTTCTGTGTGAGCACTGTGTGGCAGGTGC	2038
OY	2032	TTTTCCTATTCACAGAGGTGTGTGTGTGTGTGTGTGGGTGTG	2069
Db	2039	TTTTCCTATTCACAGAGGTG	2076
RESULT 7			
US-09-824-807-1			
Sequence 1, Application US/09824807			
Patent No. US20020094966A1			
GENERAL INFORMATION:			
APPLICANT: Serrero, GINETE			
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS			
FILE REFERENCE: Z5996.488/P001-A			
CURRENT APPLICATION NUMBER: US/09/824,807			
CURRENT FILING DATE: 2001-04-04			
PRIOR APPLICATION NUMBER: 08/991,862			
PRIOR FILING DATE: 1997-12-16			
PRIOR APPLICATION NUMBER: 08/863,862			
PRIOR FILING DATE: 1997-05-23			
NUMBER OF SEQ ID NOS: 17			
SOFTWARE: PatentIn Ver. 2.0			
SEQ ID NO 1			
LENGTH: 2137			
TYPE: DNA			
ORGANISM: Mouse epithelin/granulin			

```

1 RESULT 7 -807-1
2 US-09-824-807-1
3 : Sequence 1, Application US/09824807
4 : Patent No. US20020094966A1
5 : GENERAL INFORMATION:
6 : APPLICANT: Serrero, GINETTE
7 : TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
8 : FILE REFERENCE: Z5956.488/P001-A
9 : CURRENT APPLICATION NUMBER: US/09/824, 807
10 : CURRENT FILING DATE: 2001-04-04
11 : PRIOR APPLICATION NUMBER: 08/991,862
12 : PRIOR FILING DATE: 1997-12-16
13 : PRIOR APPLICATION NUMBER: 08/863,862
14 : PRIOR FILING DATE: 1997-05-23
15 : NUMBER OF SEQ ID NOS: 17
16 : SOFTWARE: Patentln Ver. 2.0
17 : SEQ ID NO 1
18 : LENGTH: 2137
19 : TYPE: DNA
20 : ORGANISM: Mouse epithelin/granulin

```

; ORGANISM: mouse epithelin/granulin

FEATURE:
NAME/KEY: CDS
LOCATION: (23) ..(1789)
OTHER INFORMATION: The sequence is identical to that of the published
OTHER INFORMATION: mouse granuln except for one nucleotide (T
OTHER INFORMATION: instead of G) at position 1071 of GP88 cDNA
OTHER INFORMATION: (position 1056 of mouse granuln).
US-09-824-807-1

Query Match 57.3%; Score 1200; DB 10; Length 2137;
Best Local Similarity 75.6%; Pred. No. 8e-315;
Matches 1572; Conservative 0; Mismatches 485; Indels 21; Gaps 6;

QY 1 CGCAGCAGACATGTCGACCTGTCGAGCTGGTGCCCTTAACAGAGGCTGTGGCT 60
DB 11 CGCAGCAGACATGTCGAGCTGTGATGAGCTGGTGCCCTTCGGGAGGCTGTGGCT 70
QY 61 GGAACGCGTGCCAGATGTCAGTTCGCTGCTGGCTGTGCTGGACCCCGAGGA 120
DB 71 GGAACAGAGTTCAGATGTCGAGTTCGCTGCTGGCTGTGCTGGACCCCGAGGA 130
QY 121 GCCAGTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 131 GCCAGTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 190
QY 181 CTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 191 CTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 250
QY 241 GTCTCAGGACTTCAGATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 251 GTCTCAGGACTTCAGATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 310
QY 301 CACTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 311 CACTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 370
QY 361 GGTACACTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 371 G---ATAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 427
QY 421 TCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 428 GGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 487
QY 481 TGCCTGAGAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 488 TGCCTGAGAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
QY 541 CGCTGATACACCAACGAGGACCAACCCCTGAGCAAGAGCTCCCTGCGAGAGACT 600
DB 548 CGATGCTTACACCAACGAGGACCAACCCCTGAGCAAGAGCTCCCTGCGAGAGACT 607
QY 601 AACAGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 608 AACAGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 667
QY 661 GATGTTTACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 668 GATGTTTACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 727
QY 721 GCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 728 GCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 787
QY 781 CAGAGTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 788 CAGAGTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 844
QY 841 CACACAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 845 TACCCAGTGAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 904

QY 901 TCCGCTCTACAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 905 TCCGCTCTACAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 964
QY 961 GACCACTATACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 965 GATCAGTATACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1024
QY 1021 CAGGAGCCCAACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1025 ATGGGTATCTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1084
QY 1081 CCACAGTGTGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1085 CCACAGTGTGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1144
QY 1141 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 1145 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1204
QY 1201 TGCCTGAGACCAACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1205 TGCCTGAGACCAACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1264
QY 1261 CAGGAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1265 CAGGAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1324
QY 1321 TCCACCCCAACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1325 TCCACCCCAACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1384
QY 1381 TGCCTGAGACCAACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1385 TGCCTGAGACCAACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1444
QY 1441 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1445 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1504
QY 1501 AAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
DB 1505 AAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1561 AAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
DB 1561 --GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1618
QY 1621 AACGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
DB 1619 AACGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1678
QY 1681 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
DB 1679 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1738
QY 1741 GCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
DB 1739 ATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1798
QY 1801 GTACTGAA-----GACTGTGACAGCTGCTGCTGCTGCTGCTGCTGCT 1853
DB 1799 GTACTGAA-----GACTGTGACAGCTGCTGCTGCTGCTGCTGCTGCT 1858
QY 1854 AGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1912
DB 1859 AGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1918
QY 1913 ATCAGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1971
DB 1919 ATCAGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1978
QY 1972 CAAAAGCCATTTACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2031

Db 1979 CAAAAGCCCCGATATCAAACTGCTATTTCTTCCGTTTCTGTGACCTGTGTGCGCAGGTGC 2038
QY 2032 TTTTCCCTATCCACAGGGGTTTGTGTGTGTGTTGGTGTG 2069
Db 2039 TCTTCCCGAGCCACAGGTGTGTGTGTGAGCTTGTGTG 2076

RESULT 8

US-09-884-441-89/c
; Sequence 89, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 89
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)...(561)
; OTHER INFORMATION: n = A,T,C or G
US-09-884-441-89

Query Match 23.1%; Score 483.8; DB 10; Length 561;
Best Local Similarity 97.7%; Pred. No. 2.4e-121;
Matches 521; Conservative 0; Mismatches 9; Indels 3; Gaps 3;

QY 1530 CTTCCTGCCCCCTACCCCTCAGCTGGGTGTGAAGACGCTGGAGTGTGGGGAAGACACTT 1589
Db 561 CTTCCTGCCCCCTACCCCTCAGCTGGGTGTGAAGACGCTGGAGTGTGGGGAAGACACTT 503
QY 1590 CTGCATATATAACAGACCTGCTGCGGAGACAAACGAGGCTGGGCTGTGTGACCTTA 1649
Db 502 CTGCATATATAACAGACCTGCTGCGGAGACAAACGAGGCTGGGCTGTGTGACCTTA 443
QY 1650 GCCCAGGAGGCTGT 1709
Db 442 CCGCAGGAGGCTGT 383
QY 1710 ACGCAGGAGGCTGT 1769
Db 382 ACGCAGGAGGCTGT 323
QY 1770 CCCAGCTTGAAGACAGT 1829
Db 322 CCCAGCTTGAAGACAGT 263
QY 1830 CCAGCTGAGAGGCTGT 1889
Db 262 CCAGCTGAGAGGCTGT 203
QY 1890 CTGGAGCCCCCTTGTAGTCTCCCATCACCATTGAGGAGTGGGCTGCAATCTTAAG-CCCTT 1949
Db 202 CTGGAGCCCCCTTGTAGTCTCCCATCACCATTGAGGAGTGGGCTGCAATCTTAAG-CCCTT 144
QY 1950 CCTTGTCAAGAGGGGTTGAGGCAAAAGCC-CATTACAAGTGCATCCCTCCCGCTT 2008
Db 143 CCTTGTCAAGAGGGGTTGAGGCAAAAGCC-CATTACAAGTGCATCCCTCCCGCTT 84
QY 2009 CAGTGAACCTGT 2061
Db 83 CAGTGAACCTGT 31

RESULT 9
US-09-884-441-90/c
; Sequence 90, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 90
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-884-441-90

Query Match 18.2%; Score 381.2; DB 10; Length 561;
Best Local Similarity 99.2%; Pred. No. 1.4e-93;
Matches 383; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGGACAGCATGTGACCTGCTGTGAGCTGGTGGCTTAAACAGACAGGCTGTGTGCT 60
Db 390 CGCAGGACAGCATGTGACCTGCTGTGAGCTGGTGGCTTAAACAGACAGGCTGTGTGCT 331
QY 61 GGAAGCGGCTGCGCAGATGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
Db 330 GGAAGCGGCTGCGCAGATGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 271
QY 121 GCCAGTACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 270 GCCAGTACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 211
QY 181 CTGGGTGCCCCCTGCCAGTGTATGATGCCACTGTGCTGCTGCTGCTGCTGCTGCTGCTTACC 240
Db 210 CTGGGTGCCCCCTGCCAGTGTATGATGCCACTGTGCTGCTGCTGCTGCTGCTGCTGCTTACC 151
QY 241 GTCAGGAGCTTCAAGT 300
Db 150 GTCAGGAGCTTCAAGT 91
QY 301 CACTGTGCCCCAGGGGCTTCCACTGACAGTGTGAGAGGAGGAGTGTGTGTGTGTGTGTGTGT 360
Db 90 CACTGTGCCCCAGGGGCTTCCACTGACAGTGTGAGAGGAGGAGTGTGTGTGTGTGTGTGTGT 31
QY 361 GGTAAACACTCCGTGGGTGTCATCCA 386
Db 30 GGTAAACACTCCGTGGGTGTCATCCA 5

RESULT 10

US-09-960-352-6772
; Sequence 6772, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Neangth
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(102983C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 6772
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 29-LIB34-003-Q1-E1-H9

US-09-960-352-6772

Query Match 12.9%; Score 270.4; DB 10; Length 400;
Best Local Similarity 81.8%; Pred. No. 1.1e-63;
Matches 324; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

OY 1 CGCAGGACACCATGTGACCTGTGTGAGCTGGTGGCCCTTAACAGCAGGCGTGTGGCT 60
DB 4 CGCAGGACACCATGTGACCTGTGTGAGCTGGTGGCCCTTAACAGCAGGCGTGTGGCT 63
OY 61 GGAACGCGGTGCCAGATGTGTGATGCTGCTGGCCCTGTGGCTGTGACCCCGGAGAGA 120
DB 64 GGAACGCGGTGCCAGATGTGTGATGCTGCTGGCCCTGTGGCTGTGACCCCGGAGAGA 123
OY 121 GCCAGCTACAGCTGTGCGCTGCTGCTGTGACAAATGAGCCCAACACTGAGACAGCAT 180
DB 124 GCCAGCTACAGCTGTGCGCTGCTGCTGTGACAAATGAGCCCAACACTGAGACAGCAT 183
OY 181 CTGGGTGGCCCTGCGCAGGTGATGCTGCTGCTGCGCCACTCTGTGACTTTTACC 240
DB 184 CTGGGTGGCCCTGCGCAGGTGATGCTGCTGCTGCGCCACTCTGTGACTTTTACC 243
OY 241 GTCGTAGGAGCTTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 244 GTCGTAGGAGCTTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303
OY 301 CACTGTGCGCCAC- GGGGCTTCCACTGACAGTGCAGAGCGGCGATCTGCTCCAAAGATC 359
DB 304 CACTGTGCGCCAC- GGGGCTTCCACTGACAGTGCAGAGCGGCGATCTGCTCCAAAGATC 363
OY 360 AGGTAAACAATCTCGTGGTGGTCCATTCAGTGGCTTGA 395
DB 364 AGGTAAACAATCTCGTGGTGGTCCATTCAGTGGCTTGA 399

RESULT 11

US-09-960-352-9598
; Sequence 9598, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Mengling
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9598
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 41-LIB34-036-Q1-E1-C2
US-09-960-352-9598

Query Match 11.3%; Score 236.4; DB 10; Length 398;
Best Local Similarity 79.7%; Pred. No. 1.8e-54;
Matches 279; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

OY 1 CGCAGGACACCATGTGACCTGTGTGAGCTGGTGGCCCTTAACAGCAGGCGTGTGGCT 60
DB 49 CGCAGGACACCATGTGACCTGTGTGAGCTGGTGGCCCTTAACAGCAGGCGTGTGGCT 108
OY 61 GGAACGCGGTGCCAGATGTGTGATGCTGCTGGCCCTGTGGCTGTGACCCCGGAGAGA 120
DB 109 GGAACGCGGTGCCAGATGTGTGATGCTGCTGGCCCTGTGGCTGTGACCCCGGAGAGA 168
OY 121 GCCAGCTACAGCTGTGCGCTGCTGCTGTGACAAATGAGCCCAACACTGAGACAGCAT 180
DB 169 GCCAGCTACAGCTGTGCGCTGCTGCTGTGACAAATGAGCCCAACACTGAGACAGCAT 228

OY 181 CTGGGTGGCCCTGCCAGGTTGATGCCACTGCTGCGCGCCACTCTGTGACTTTTACC 240
DB 229 CTGGGTGGCCCTGCCAGGTTGATGCCACTGCTGCGCGCCACTCTGTGACTTTTACC 288
OY 241 GTCGTAGGAGCTTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 289 GTCGTAGGAGCTTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 348
OY 301 CACTGTGCGCCAC- GGGGCTTCCACTGACAGTGCAGAGCGGCGATCTGCTCCAAAGATC 350
DB 349 CACTGTGCGCCAC- GGGGCTTCCACTGACAGTGCAGAGCGGCGATCTGCTCCAAAGATC 398

RESULT 12

US-09-864-761-27557/C
; Sequence 27557, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 27557
; LENGTH: 233
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC003043.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.65
; OTHER INFORMATION: SWISSPROT HIT: P28799, EVALU6 7.00e-47

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 21, 2003, 13:05:13 : Search time 98 Seconds
(without alignments)
6555.998 Million cell updates/sec

Title: US-08-991-862-16

Perfect score: 2095
Sequence: 1 cgcagcgagcagcattgtgac.....atgaattgtcattctt 2095

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA: *
1: /cgn2_6/ptodata/1/lna/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/lna/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/lna/5A.COMB.seq: *
4: /cgn2_6/ptodata/1/lna/5B.COMB.seq: *
5: /cgn2_6/ptodata/1/lna/PCITUS.COMB.seq: *
6: /cgn2_6/ptodata/1/lna/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2095	100.0	2095	4	US-08-991-862-16
2	1756.6	83.8	1779	1	US-07-668-648-3
3	1756.6	83.8	1779	2	US-08-429-998-3
4	1756.6	83.8	1779	2	US-08-431-333-3
5	1756.6	83.8	1779	5	PCR-US91-02321-3
6	1200	57.3	2137	4	US-08-991-862-1
7	1142.6	54.5	1767	1	US-07-668-648-1
8	1142.6	54.5	1767	2	US-08-429-998-1
9	1142.6	54.5	1767	2	US-08-431-333-1
10	1142.6	54.5	1767	5	PCR-US91-02321-1
11	1107.4	52.9	1767	1	US-07-668-648-5
12	1107.4	52.9	1767	2	US-08-429-998-5
13	1107.4	52.9	1767	2	US-08-431-333-5
14	1107.4	52.9	1767	5	PCR-US91-02321-5
15	483.8	23.1	561	4	US-09-404-879A-89
16	396.8	18.9	539	1	US-07-668-648-7
17	396.8	18.9	539	2	US-08-429-998-7
18	396.8	18.9	539	2	US-08-431-333-7
19	396.8	18.9	539	5	PCR-US91-02321-7
20	381.2	18.2	561	4	US-09-404-879A-90
21	139	6.6	561	4	US-09-404-879A-90
22	72.6	3.5	341	1	US-07-668-648-9
23	72.6	3.5	341	2	US-08-429-998-9
24	72.6	3.5	341	2	US-08-431-333-9
25	72.6	3.5	341	5	PCR-US91-02321-9
26	39.2	1.9	1926	4	US-09-249-585A-2
27	39.2	1.9	2580	3	US-09-050-863-2

C	28	39.2	1.9	2580	4	US-09-359-081-2	Sequence 2, Appl
C	29	39.2	1.9	5452	2	US-09-130-114-1	Sequence 1, Appl
C	30	39.2	1.9	9600	4	US-08-910-647-1	Sequence 1, Appl
C	31	39.2	1.9	9600	4	US-09-620-925-1	Sequence 1, Appl
C	32	39.2	1.9	10596	1	US-07-884-811-15	Sequence 15, Appl
C	33	39.2	1.9	10596	1	US-07-885-971-15	Sequence 15, Appl
C	34	39.2	1.9	10596	1	US-08-087-783A-15	Sequence 15, Appl
C	35	39.2	1.9	10596	1	US-08-194-088B-15	Sequence 15, Appl
C	36	39.2	1.9	10596	2	US-08-194-087-15	Sequence 15, Appl
C	37	39.2	1.9	10596	5	PCR-US93-04648-15	Sequence 15, Appl
C	38	38.4	1.8	7218	1	US-08-232-463-14	Sequence 14, Appl
C	39	38	1.8	2742	3	US-08-911-853-16	Sequence 16, Appl
C	40	38	1.8	2742	4	US-09-479-409-16	Sequence 16, Appl
C	41	38	1.8	17612	3	US-08-479-453-16	Sequence 16, Appl
C	42	38	1.8	17612	4	US-08-911-853-29	Sequence 29, Appl
C	43	38	1.8	17612	4	US-09-479-453-29	Sequence 29, Appl
C	44	38	1.8	17612	4	US-09-479-453-29	Sequence 29, Appl
C	45	37.6	1.8	3183	1	US-08-849-212-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-991-862-16
; Sequence 16, Application US/08991862
; Patent No. 6309826
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.488/P001-A
; CURRENT APPLICATION NUMBER: US/08/991,862
; EARLIER FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/863,862
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Human GP88 CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(1791)
; OTHER INFORMATION: Nucleotide sequence of human granuln/epithelin
; OTHER INFORMATION: Precursor (human GP88). Human Granulin Genebank
; OTHER INFORMATION: M75161.
US-08-991-862-16

Query Match 100.0%; Score 2095; DB 4; Length 2095;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2095; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CGCAGCGAGCAGCATGTGAGCCTGTGAGCTGGGTGACCTTAACAGAGGGCTGTGCT	60
DB	1	CGCAGCGAGCAGCATGTGAGCCTGTGAGCTGGGTGACCTTAACAGAGGGCTGTGCT	60
QY	61	GGAACGGGGGCCAGATGTCAGTTCTGCGGCTGCGCTGAGCCCGGAGGA	120
DB	61	GGAACGGGGGCCAGATGTCAGTTCTGCGGCTGCGCTGAGCCCGGAGGA	120
QY	121	GCCAGCTACAGCTGCTGCCCTCTTGAGACAATGCGCCCAACACTGACAGGACAT	180
DB	121	GCCAGCTACAGCTGCTGCCCTCTTGAGACAATGCGCCCAACACTGACAGGACAT	180
QY	181	CTGGGTGGCCCTGCTGAGTTGATGCCACTGCTCTGCGGGCACTGCTGATTTACC	240
DB	181	CTGGGTGGCCCTGCTGAGTTGATGCCACTGCTCTGCGGGCACTGCTGATTTACC	240
QY	241	GTCACAGGAGCTTCAGATTCTGCGCCCTCCAGAGAGCCGTGGCATGGGGATGGCCAT	300
DB	241	GTCACAGGAGCTTCAGATTCTGCGCCCTCCAGAGAGCCGTGGCATGGGGATGGCCAT	300

OY	301	CACGTCGCCACGAGGGCTTCACATGCAATGACAGAGGGGAAATCCGCTTCCAAAGATCA	360
Db	301	CACGTCGCCACGAGGGCTTCACATGCAATGACAGAGGGGAAATCCGCTTCCAAAGATCA	360
OY	361	GGTAAACAATCCGTTGGGTGCCATTCACATGCGCCCTGATAGTCAAGTTGGAAATGCCGGACTTC	420
Db	361	GGTAAACAATCCGTTGGGTGCCATTCACATGCGCCCTGATAGTCAAGTTGGAAATGCCGGACTTC	420
OY	421	TCCAAGTGCCTGTGTTAATGATGATAGGTGCTCTGGGGGGTGTCTGCCCATATGCCACAGCTTCC	480
Db	421	TCCAAGTGCCTGTGTTAATGATGATAGGTGCTCTGGGGGGTGTCTGCCCATATGCCACAGCTTCC	480
OY	481	TGCTGTGAAGACAGAGGGTGCATGCTGTGCCACAGGGTGCCTTCGCGACCTGGTTACACAC	540
Db	481	TGCTGTGAAGACAGAGGGTGCATGCTGTGCCACAGGGTGCCTTCGCGACCTGGTTACACAC	540
OY	541	CGCTGCATCACACCCACAGGGCACCCACCCCTGGCCAAAGACTCCCTCCGACAGAGACT	600
Db	541	CGCTGCATCACACCCACAGGGCACCCACCCCTGGCCAAAGACTCCCTCCGACAGAGACT	600
OY	601	AACAGGCGATGGCCTTGTCCAGCTCGGTATGTGTCCGAGCGACAGGGTCCCGGTGCCCT	660
Db	601	AACAGGCGATGGCCTTGTCCAGCTCGGTATGTGTCCGAGCGACAGGGTCCCGGTGCCCT	660
OY	661	GATGGTTCTACCTGCTGTGAGCTGCCACAGGGGAATATAGGTTGGTGGCCCATATGGCCACAC	720
Db	661	GATGGTTCTACCTGCTGTGAGCTGCCACAGGGGAATATAGGTTGGTGGCCCATATGGCCACAC	720
OY	721	GCCACCTGCTGCTCCGATTCACCTGCATGCTGCCGCCCAAGACACTGTGTATACCTGATC	780
Db	721	GCCACCTGCTGCTCCGATTCACCTGCATGCTGCCGCCCAAGACACTGTGTATACCTGATC	780
OY	781	CAGAGTAAATGTCCTCTCCAAAGAGAAACGCTACACGACTCCTCACTAACTGGCTGCG	840
Db	781	CAGAGTAAATGTCCTCTCCAAAGAGAAACGCTACACGACTCCTCACTAACTGGCTGCG	840
OY	841	CACACAGTGGGCGATGTGAATGTGCATGTAGATGAGTGGCCCGAGATGGCTATACCTGC	900
Db	841	CACACAGTGGGCGATGTGAATGTGCATGTAGATGAGTGGCCCGAGATGGCTATACCTGC	900
OY	901	TGCGGTACACAGTGGGGGGCTGTGGGCTGCTGCCCTTAAACCAAGCTGTGTGCTGTAG	960
Db	901	TGCGGTACACAGTGGGGGGCTGTGGGCTGCTGCCCTTAAACCAAGCTGTGTGCTGTAG	960
OY	961	GACCAATACACTGCTCTCCCGGGGGTTTACGTGTGACACGAGAGGGTACCTGTGAA	1020
Db	961	GACCAATACACTGCTCTCCCGGGGGTTTACGTGTGACACGAGAGGGTACCTGTGAA	1020
OY	1021	CAGGGGCCCCACAGGTGGCCCTGGATGAGAAAGGCCACAGCTACCTCAAGCTCGCCACAC	1080
Db	1021	CAGGGGCCCCACAGGTGGCCCTGGATGAGAAAGGCCACAGCTACCTCAAGCTCGCCACAC	1080
OY	1081	CCACAAGCTTGAAGAGAGATGTGCCCTGTGATAATGTACAGAGCTGTCCCTCCATGCAT	1140
Db	1081	CCACAAGCTTGAAGAGAGATGTGCCCTGTGATAATGTACAGAGCTGTCCCTCCATGCAT	1140
OY	1141	ACCTGCTGCCAATCTCACGTTGTGGGAGATGGGGCTGTGTCATATCCACAGAGCTGTGTC	1200
Db	1141	ACCTGCTGCCAATCTCACGTTGTGGGAGATGGGGCTGTGTCATATCCACAGAGCTGTGTC	1200
OY	1201	TGCTGTGAGCCACAGCACTGCTCTCCCCCAAGCTTACATCACTGTGTAGCTGAGGGGACAGT	1260
Db	1201	TGCTGTGAGCCACAGCACTGCTCTCCCCCAAGCTTACATCACTGTGTAGCTGAGGGGACAGT	1260
OY	1261	CAGGAGGAAACGAGATCTGTGCGCTGTGAGCTGTGAATAATCTGTGCCGCGCGGTTCTTTA	1320
Db	1261	CAGGAGGAAACGAGATCTGTGCGCTGTGAGCTGTGAATAATCTGTGCCGCGCGGTTCTTTA	1320
OY	1321	TCCACACCCACAGACATCTGGCTGTGACACACACACAGCTGGCCGCTGGCGGAACCTGC	1380
Db	1321	TCCACACCCACAGACATCTGGCTGTGACACACACACAGCTGGCCGCTGGCGGAACCTGC	1380
OY	1381	TGCCCGACCCAGGGTGGGACTTGCGCTGTGCTCCAGTTGCCCATGCTGTGTGTGCTGGAG	1440
Db	1381	TGCCCGACCCAGGGTGGGACTTGCGCTGTGCTCCAGTTGCCCATGCTGTGTGTGCTGGAG	1440

```

Db      1381  TCCCCGAGCCAGGGGTGGGAGCTGGGCCCTGCTGCACATTGCCCCATGCTGTGTGCTGGCAG 1440
QY      1441  GATCGCCAGCACTGCTACC GGCGTGGCTGCTACACCTGCACAACGTGAAGGCTGATCTGCGAG 1500
Db      1441  GATCGCCAGCACTGCTACC GGCGTGGCTGCTACACCTGCACAACGTGAAGGCTGATCTGCGAG 1500
QY      1501  AAGGAAGTGTCCTGTGCC CAGACCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1560
Db      1501  AAGGAAGTGTCCTGTGCC CAGACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1560
QY      1561  AAGCAGCTGGAGTGTGGG GAAGAAGACATTGTGCATGATTAACAGACCGTGGCGCGAGAC 1620
Db      1561  AAGCAGCTGGAGTGTGGG GAAGAAGACATTGTGCATGATTAACAGACCGTGGCGCGAGAC 1620
QY      1621  AACCGACAGGGCTGGGC CTGCTGTCCCTAACGCCCAAGGGCGTGTGTGTGCTGATCGCGC 1680
Db      1621  AACCGACAGGGCTGGGC CTGCTGTCCCTAACGCCCAAGGGCGTGTGTGTGCTGATCGCGC 1680
QY      1681  CACTGCTCTCTGCTGTG CCTTCGCTGCGACGACGACGAGGGGTACCAAGTTGTTGCGCAGGAG 1740
Db      1681  CACTGCTCTCTGCTGTG CCTTCGCTGCGACGACGAGGGGTACCAAGTTGTTGCGCAGGAG 1740
QY      1741  GCCCGCGCTGGGAGGCC CTTTGAGGGACCCAGCTTAGAAGACGTGCTGTGAGGGACA 1800
Db      1741  GCCCGCGCTGGGAGGCC CTTTGAGGGACCCAGCTTAGAAGACGTGCTGTGAGGGACA 1800
QY      1801  GTACTGAAGACTGTGCAG ACCCTGCGGAGCCCACTGCGAGGGGTGCCCTGTGCTCAGAGCTTC 1860
Db      1801  GTACTGAAGACTGTGCAG ACCCTGCGGAGCCCACTGCGAGGGGTGCCCTGTGCTCAGAGCTTC 1860
QY      1861  CCTAGCACTCTCCCCTT ACACAAATTTCTCCCTGAGCCCATTTCTGAGCTCCCATCACAT 1920
Db      1861  CCTAGCACTCTCCCCTT ACACAAATTTCTCCCTGAGCCCATTTCTGAGCTCCCATCACAT 1920
QY      1921  GGGAGGTGGGGCTCATA TTGAAGGCCCTTCCCTGATAGAAAGGGGGTTAGAGCAAAAGGCC 1980
Db      1921  GGGAGGTGGGGCTCATA TTGAAGGCCCTTCCCTGATAGAAAGGGGGTTAGAGCAAAAGGCC 1980
QY      1981  ATTACAAGCTCCATPCC CTTCCCGCTTTCAGTGGACCCCTGTGGCCAGAGTGCTTTTCCCTA 2040
Db      1981  ATTACAAGCTCCATPCC CTTCCCGCTTTCAGTGGACCCCTGTGGCCAGAGTGCTTTTCCCTA 2040
QY      2041  TTCACAGGGGTGTTTGT GTGTGTGGGTGCTTTCATATAAGTTGTCACTTCTT 2095
Db      2041  TTCACAGGGGTGTTTGT GTGTGTGGGTGCTTTCATATAAGTTGTCACTTCTT 2095

RESULT 2
; US-07-668-3
; Sequence 3, Application US/07668648
; Patent No. 5416192
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; TITLE OF INVENTION: EPIHELINS: NOVEL CYSTEINE-RICH GROWTH
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/668,648
; FILING DATE: 19910819

```


Db	1321	GACATCGGCTGTATACACGACACACCAGCTGCCCGGTGGGAGAACCTGCTGCCCGAGCTTG	1380
Qy	1393	GGTGGAGATGGGGCTTCCTGCCAGTTGCCCATGCTGTGTGTGCGAGAGATGCCAGAC	1452
Db	1381	GGTGGAGATGGGGCTTCCTGCCAGTTGGCCCATGCTGTGTGTGCGAGAGATGCCAGAC	1440
Qy	1453	TGCTGCCCGGCTGGCTACCTTCGCAACGTGAGAGCTGCATCTCTGGAGAGAGAGTGGTC	1512
Db	1441	TGCTGCCCGGCTGGCTACCTTCGCAACGTGAGAGCTGCATCTCTGGAGAGAGAGTGGTC	1500
Qy	1513	TCTGCCGAGCTGGCACCTTCGTGGGCCGTAGCCCTCAGTGGGTGTGAAGAGCTGGAG	1572
Db	1501	TCTGCCGAGCTGGCACCTTCGTGGGCCGTAGCCCTCAGTGGGTGTGAAGAGCTGGAG	1560
Qy	1573	TGTGGGAGAGACACTTCCTGCATGATTAACAGAACCTGTGTCGGAGACAAACGACAGAGGC	1632
Db	1561	TGTGGGAGAGACACTTCCTGCATGATTAACAGAACCTGTGTCGGAGACAAACGACAGAGGC	1620
Qy	1653	TGGGCTCGCTGTCCCTACACGCCACAGGGCGTGTGTGTGCTGATCGCGCCACTGCTGTCTCT	1692
Db	1621	TGGGCTCGCTGTCCCTACACGCCACAGGGCGTGTGTGTGCTGATCGCGCCACTGCTGTCTCT	1680
Qy	1693	GCTGGCTTCGCTCGCAGCAGCGAGGGGTACCAAGTGTTCGCGAGGAGAGGCCCGCGCTGG	1752
Db	1681	GCTGGCTTCGCTCGCAGCAGCGAGGGGTACCAAGTGTTCGCGAGGAGAGGCCCGCGCTGG	1740
Qy	1753	GAGCGCCCTTTGAGAGGACCAAGCTTGAGACAGCTCTG	1791
Db	1741	GAGCGCCCTTTGAGAGGACCAAGCTTTGAGACAGCTCTG	1779

```

1      RESULT 4
2      US-08-431-333-3
3      : Sequence 3, Application US/0841333
4      : Patent No. 5965723
5      : GENERAL INFORMATION:
6      : APPLICANT: Shoyab, Mohammed
7      : APPLICANT: Plozman, Gregory D.
8      : TITLE OF INVENTION: EPTHELINS: NOVEL CYSTEINE-RICH GROWTH
9      : TITLE OF INVENTION: MODULATING PROTEINS
10     : NUMBER OF SEQUENCES: 12
11     : CORRESPONDENCE ADDRESS:
12     : ADDRESSEE: Pennie & Edmonds
13     : STREET: 1155 Avenue of the Americas
14     : CITY: New York
15     : STATE: New York
16     : COUNTRY: USA
17     : ZIP: 10036
18     : COMPUTER READABLE FORM:
19     : MEDIUM TYPE: Floppy disk
20     : COMPUTER: IBM PC compatible
21     : OPERATING SYSTEM: PC-DOS/MS-DOS
22     : SOFTWARE: Patentin Release #1.0, Version #1.25
23     : CURRENT APPLICATION DATA:
24     : APPLICATION NUMBER: US/08/431,333
25     : FILING DATE: 27-APR-1995
26     : CLASSIFICATION: 536
27     : PRIOR APPLICATION DATA:
28     : APPLICATION NUMBER: US 07/668,648
29     : FILING DATE: 13-MAR-1991
30     : ATTORNEY/AGENT INFORMATION:
31     : NAME: Miarock, S. Leslie
32     : REGISTRATION NUMBER: 18,872
33     : REFERENCE/DOCKET NUMBER: 5624-161-999
34     : TELECOMMUNICATION INFORMATION:
35     : TELEPHONE: (212)790-9090
36     : TELEFAX: (212) 869-9741
37     : INFORMATION FOR SEQ. ID NO: 3:
38     : SEQUENCE CHARACTERISTICS:
39     : LENGTH: 1779 base pairs
40     : TYPE: nucleic acid
41     : STRANDEDNESS: single
42     :
43     :
44     :
45     :
46     :
47     :
48     :
49     :
50     :
51     :
52     :
53     :
54     :
55     :
56     :
57     :
58     :
59     :
60     :
61     :
62     :
63     :
64     :
65     :
66     :
67     :
68     :
69     :
70     :
71     :
72     :
73     :
74     :
75     :
76     :
77     :
78     :
79     :
80     :
81     :
82     :
83     :
84     :
85     :
86     :
87     :
88     :
89     :
90     :
91     :
92     :
93     :
94     :
95     :
96     :
97     :
98     :
99     :
100    :

```

```

; ; TOPOLOGY: linear
; ; MOLECULE TYPE: cDNA
; ; ORIGINAL SOURCE:
; ; ORGANISM: Homo sapiens
; ; TISSUE TYPE: Kidney
; ;
; ; FEATURE:
; ; NAME/KEY: CDS
; ; LOCATION: 1..1779
; ;
; ; US-08-431-333-3

```

Query Match	83.8%;	Score 1756.6;	DB 2;	Length 1779;
Best Local Similarity	99.2%;	Pred. No. 0;		
Matches 1765; Conservative	0;	Mismatches 14;	Indels 0;	Gaps 0;

QY	13	ATGTGACCCTGGGTAGCTGGGTGGGCTTTACACACAGGGCGGTGGTGGAAAGCGGGTGC	72
Db	1	ATGTGGACCCCTGTGTAGCTGGGTGGGCTTTAACACAGGGGCTGTGTGGTGGAAAGCGGGTGC	60
QY	73	CCAGATGGTTCAGATTCGCCCCTGTGTGGCTGTGCTGGAGCCCGGAGAGGACAGCTACAGC	132
Db	61	CCAGATGGTTCAGATTCGCCCCTGTGTGGCTGTGCTGGAGCCCGGAGAGGACAGCTACAGC	120
QY	133	TGCTTCCGCTCCCTTCTGTGGAAATATGGCCCAACACTGAGACAGGACTGTGGGTGGCCCC	192
Db	121	TGCTTCCGCTCCCTTCTGTGGAAATATGGCCCAACACTGAGACAGGACTGTGGGTGGCCCC	180
QY	193	TGCCAGTTGATATGCCCATCTGCTTGCGGGCACTCTGCACTCTTTACCCTTCAGGGACT	252
Db	181	TGCCAGTTGATATGCCCATCTGCTTGCGGGCACTCTGCACTCTTTACCCTTCAGGGACT	240
QY	253	TCCAGTTGCTGCCCCCTTCCACAGAGCCGTGGCATATGGGGATGGCCATCACTGCTGCCA	312
Db	241	TCCAGTTGCTGCCCCCTTCCACAGAGCCGTGGCATATGGGGATGGCCATCACTGCTGCCA	300
QY	313	CGGGCTTCACATGACAGACAGACGGGGAGCTGCTTCCAAATATAGGTAACAACTCC	372
Db	301	CGGGCTTCACATGACAGACAGACGGGGAGCTGCTTCCAAATATAGGTAACAACTCC	360
QY	373	GTGGGTGCCATTCAGATGCCCCATAGTTCGAATGCCCGGACTTCTCCACGTGCTGT	432
Db	361	GTGGGTGCCATTCAGATGCCCCATAGTTCGAATGCCCGGACTTCTCCACGTGCTGT	420
QY	433	GTTATGGTCGATGGCTCTCTGGGGGTGCTGGCCCCATGGCCCCAGGCTTCTGTCTGTAAGAC	492
Db	421	GTTATGGTCGATGGCTCTCTGGGGGTGCTGGCCCCATGGCCCCAGGCTTCTGTCTGTAAGAC	480
QY	493	AGGGTGCACGTGTCGCCACAGGTGCTTGTGCACACTGTGTTCACACCCGCTGCATACA	552
Db	481	AGGGTGCACGTGTCGCCACAGGTGCTTGTGCACACTGTGTTCACACCCGCTGCATACA	540
QY	553	CCACAGGGACACCCCTGTGGCAAGAAAGTCTCCTGTGCCACAGAGACTAACAGGGCAGTG	612
Db	541	CCACAGGGACACCCCTGTGGCAAGAAAGTCTCCTGTGCCACAGAGACTAACAGGGCAGTG	600
QY	613	GCCCTGTCCAGTGGGTGATATGTGCCAGACAGGGTCCCGGTGGCCCTGATGGTTTCAAC	672
Db	601	GCCCTGTCCAGTGGGTGATATGTGCCAGACAGGGTCCCGGTGGCCCTGATGGTTTCAAC	660
QY	673	TGCTGTGAGCTGCCAGTGGGAAATATATGGCTGTGCCAATGTCCCAAGGCACTGCTGTGC	732
Db	661	TGCTGTGAGCTGCCAGTGGGAAATATATGGCTGTGCCAATGTCCCAAGGCACTGCTGTGC	720
QY	733	TCCGATTCACCTTGCACTGTGTGCCCCCAAGACACTGTGTGTGACTGATCCAGATTAAGTGC	792
Db	721	TCCGATTCACCTTGCACTGTGTGCCCCCAAGACACTGTGTGTGACTGATCCAGATTAAGTGC	780
QY	793	CTCTCACAAGGAAGAGCTATCACAGGAGACTCTCTCACTAAAGCTGCTGGGCACACAGTGGC	852
Db	781	CTCTCACAAGGAAGAGCTATCACAGGAGACTCTCTCACTAAAGCTGCTGGGCACACAGTGGG	840
QY	853	GATGTGAATGTGACATGGAGGTAGCTGCCAGATGGCTATACCTGCTCCGCTTACAG	912
Db	841	GATGTGAATGTGACATGGAGGTAGCTGCCAGATGGCTATACCTGCTCCGCTTACAG	900

OY	913	TCGGGAGCCTGGGGCTCGTGGCCCTTTTACCAGGCTGTGTGCTGAGGACCAACATATAC	972
Db	901	TCGGGAGCCTGGGGCTCGTGGCCCTTTTACCAGGCTGTGTGCTGAGGACCAACATATAC	960
OY	973	TGCTGTCCCGGGGGTTTTACGTGTGACACGACAGAAAGGTACCTGTGAACAGGGGCCAC	1033
Db	961	TGCTGTCCCGGGGGTTTTACGTGTGACACGACCAAAAGGTACCTGTGAACAGGGGCCAC	1020
OY	1093	CAGGTGCCCTGGATGAGAAAGGCCCGACGCTCAGCCTCGCACAACCACAGCCTTG	1097
Db	1021	CAGGTGCCCTGGATGAGAAAGGCCCGACGCTCAGCCTCGCACAACCACAGCCTTG	1080
OY	1093	AAGAGATGTCTCCCTGTGATTAATGTACAGAGCTGTCTCCCTCCCATATCCTGTCCAA	1155
Db	1081	AAGAGATGTCTCCCTGTGATTAATGTACAGAGCTGTCTCCCTCCCATATCCTGTCCAA	1140
OY	1153	CTCACGTCTGGGAGGTGGGGCTGTCTCCATATCCAGAGGCTGTCTGTCTCGACAC	1211
Db	1141	CTCACGTCTGGGAGGTGGGGCTGTCTCTCCATATCCAGAGGCTGTCTGTCTCGACAC	1200
OY	1213	CAGCACTGCTCCCCCAGACGATACAGTGTGTAGCTGAGGGGGCAGGTGACAGGAGAAC	1277
Db	1201	CAGCACTGCTCCCCCAGAGGCTACAGCTGTGTAGCTGTAGGGGAGTGTACAGGAGAAC	1260
OY	1273	GAGATCGTGGCTGGAGCTGGAAAGATGCTGCCCCGGCGGTTCTTATCCACCCAGA	1333
Db	1261	GAGATCGTGGCTGGAGCTGGAAAGATGCTGCCCCGGCGGCTTCTTATCCACCCAGA	1320
OY	1333	GACATCGCTGTGACACGACACACAGTGGCCCCGTGGGGGAACCTGTCTGCCAGACC	1397
Db	1321	GACATCGCTGTGACACGACACACAGTGGCCCCGTGGGGGACGACCTGTCTGCCAGACC	1380
OY	1393	GGTGGAGACTGGGCCCTCTGCGAATTTGCCCATAGCTGTGTGTGCTGCGAGGATGCGCAGC	1453
Db	1381	GGTGGAGACTGGGCCCTCTGCGAGTTTCCCGCATGTGTGTGTGCTGCGAGGATGCGCAGC	1440
OY	1453	TGCTGTCCCGCTGGCTACACCTGCAAGGTAAAGCTTCGATCTGTGCGAAGAAAGTGGTC	1511
Db	1441	TGCTGTCCCGCTGGCTACACCTGCAAGGTAAAGCTTCGATCTGTGCGAAGAAAGTGGTC	1500
OY	1513	TCTGTCCAGCCTGTGCACACTTCTGTGGCCCGTAGCCCTACAGTGGGTGTGAAGACGTGGAG	1577
Db	1501	TCTGTCCAGCCTGTGCACACTTCTGTGGCCCGTAGCCCTACAGTGGGTGTGAAGACGTGGAG	1560
OY	1573	TGTGGGGAAGACACTTCTGTCCATGATTAACCAACCTGCTGCCGAGACAACGACAGGGC	1633
Db	1561	TGTGGGGAAGACACTTCTGTCCATGATTAACCAACCTGCTGCCGAGACAACGACAGGGC	1620
OY	1633	TGGGCTGTGTCTCCCTACGCGCCAGAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1697
Db	1621	TGGGCTGTGTCTCCCTACGCGCCAGAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1680
OY	1693	GCTGTCTTCGCTGCGACAGCAGAGGGGTACCAATGTTTTGCGAGGAGGCCCCGGGCTGG	1753
Db	1681	GCTGTCTTCGCTGCGACAGCAGAGGGGTACCAATGTTTTGCGAGGAGGCCCCGGGCTGG	1740
OY	1753	GACGCCCCCTTGAGAGGACCAAGCCTTGAGACACTGTCTG	1791
Db	1741	GACGCCCCCTTGAGAGGACCAAGCCTTGAGACACTGTCTG	1779

RESULT 5
PCT-US91-02321-3

```
;; Sequence 3, Application PC/TUS9102321
; GENERAL INFORMATION:
```

APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory

1	TITLE OF INVENTION:	EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH
2	TITLE OF INVENTION:	MODULATING PROTEINS
3	NUMBER OF INVENTIONS:	1
4	NUMBER OF SEQUENCES:	10

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: BR14701-M

[illegible]

```

1 STREET: 3005 First Avenue
2 CITY: Seattle
3 STATE: Washington
4 COUNTRY: USA
5 ZIP: 98121
6
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Floppy disk
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: PatentIn Release #1.0, Version #1.25
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: PCT/US91/02321
14 FILING DATE: 19910403
15 CLASSIFICATION: 514
16 ATTORNEY/AGENT INFORMATION:
17 NAME: Poor, Brian W.
18 REGISTRATION NUMBER: 32,928
19 REFERENCE/DOCKET NUMBER: ON071A-PC
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: (206)728-4800
22 TELEFAX: (206)448-4775
23 INFORMATION FOR SEQ ID NO: 3:
24 SEQUENCE CHARACTERISTICS:
25 LENGTH: 1779 base pairs
26 TYPE: NUCLEIC ACID
27 STRANDEDNESS: single
28 TOPOLOGY: linear
29 MOLECULE TYPE: cdna
30 ORIGINAL SOURCE:
31 ORGANISM: Homo sapiens
32 TISSUE TYPE: kidney
33 FEATURE:
34 NAME/KEY: CDS
35 LOCATION: 1..1779
36 PCT-US91-02321-3

```

Query Match	83.88;	Score 1756.6;	DB 5;	Length 1779;
Best Local Similarity	99.28;	Pred. No. 0;		
Matches 1765; Conservative	0;	Mismatches 14;	Indels 0;	Gaps 0;

QY	13	ATGTGGACCCGTGTGAGCTGGGTGGGCTTAAACACAGGGCTGTGGCTGGAAACCGGTGC	72
Db	1	ATGTGGACCCGTGTGAGCTGGGTGGGCTTAAACACAGGGCTGTGGCTGGAAACCGGTGC	60
QY	73	CCAGATGGTCAGTTCGTGCGCTGTGTGGCTGTGCTGGACCCGGAGAGGCCACTACAGC	133
Db	61	CCAGATGGTCAGTTCGTGCGCTGTGTGGCTGTGCTGGACCCGGAGAGGCCACTACAGC	120
QY	133	TGCTGTCCCTCCCTTCTTGAGCAAAATGGCCCAACACACTGACAGGACATCTGTGGGGGGCC	192
Db	121	TGCTGTCCCTCCCTTCTTGAGCAAAATGGCCCAACACACTGACAGGACATCTGTGGGGGGCC	180
QY	193	TGCCAGTGTGATGGCCACACTGCTGTGCGGGCCACTCTTGATCTTTTAACTGCTCAGGAGCT	252
Db	181	TGCCAGTGTGATGGCCACACTGCTGTGCGGGCCACTCTTGATCTTTTAACTGCTCAGGAGCT	240
QY	253	TCCAGTTTCCTCCCTTCCAGAGAGCCGTGGCATGGGGGATGGCCATCACTGGTGGCA	312
Db	241	TCCAGTTTCCTCCCTTCCAGAGAGCCGTGGCATGGGGGATGGCCATCACTGGTGGCA	300
QY	313	CGGGGCTTCCACTGCAGTGCAGAGCGGGCGAATCTGTTTCCAAAGATAGGTAACAACTCC	372
Db	301	CGGGGCTTCCACTGCAGTGCAGAGCGGGCGAATCTGTTTCCAAAGATAGGTAACAACTCC	360
QY	373	GTGGGTGCATCCAGTGGCCCTGATATGATCAGTTGCAATGCCCGGACTTCTCCAGTGTGT	432
Db	361	GTGGGTGCATCCAGTGGCCCTGATATGATCAGTTGCAATGCCCGGACTTCTCCAGTGTGT	420
QY	433	GTTATAGTCATGGCTCCTGGGGGTGGTGGCCCAATGGCCCAAGGTTCTCTGTGTGAAGAC	492
Db	421	GTTATAGTCATGGCTCCTGGGGGTGGTGGCCCAATGGCCCAAGGTTCTCTGTGTGAAGAC	480
QY	493	AGGGTGCACGTGTCGGACAGGTGACTTGTGCGACCTGGTTTCAACCCGCTGCATACA	552

|||||
Db 481 AGGATGACCTGCTGTCGACGAGTCTTCTGAGCTGCTGACACCCGCTCATTACCA 540
|||||
Oy 553 CCCAGGGGACCCACCCTTGGCAAGAGCTCCCTGCCAGAGACTAAACAGGGCAGT 612
|||||
Db 541 CCCAGGGGACCCACCCTTGGCAAGAGCTCCCTGCCAGAGACTAAACAGGGCAGT 600
|||||
Oy 613 GCGTGTCCAGTCTGGTCTATGTGTCCGAGCAGCGGTCCCGGTGCCCTGATGGTTTACC 672
|||||
Db 601 GCGTGTCCAGTCTGGTCTATGTGTCCGAGCAGCGGTCCCGGTGCCCTGATGGTTTACC 660
|||||
Oy 673 TGGTGTGACCTGCCCCAGTGGGAAGTATGGTGTGCTGCCAATGGCCAAAGCCACTGCTGC 732
|||||
Db 661 TGGTGTGACCTGCCCCAGTGGGAAGTATGGTGTGCTGCCAATGGCCAAAGCCACTGCTGC 720
|||||
Oy 733 TCCGATCAGCTGACGTGCCCCCAAGACACTGTGTGACCTGATCCAGATTAAGTGC 792
|||||
Db 721 TCCGATCAGCTGACGTGCCCCCAAGACACTGTGTGACCTGATCCAGATTAAGTGC 780
|||||
Oy 793 CTCTCCAGAGAGAGAGCTACACAGGACCTCTCCTAAGCTGCGCTGCGACACAGTGGGC 852
|||||
Db 781 CTCTCCAGAGAGAGAGCTACACAGGACCTCTCCTAAGCTGCGCTGCGACACAGTGGGC 840
|||||
Oy 853 GATGTGAATGTACATGAGAGTGGAGTGGCTGCCAGATGGCTATACCTGCTGCTCTACAG 912
|||||
Db 841 GATGTGAATGTACATGAGAGTGGAGTGGCTGCCAGATGGCTATACCTGCTGCTCTACAG 900
|||||
Oy 913 TCGGGGGCTGGGGGCTGCTGCCCCCTTTTACCAGAGCTGTGTGCTGTGAGGACCAATACAC 972
|||||
Db 901 TCGGGGGCTGGGGGCTGCTGCCCCCTTTTACCAGAGCTGTGTGCTGTGAGGACCAATACAC 960
|||||
Oy 973 TCGTGTCCCGGGGTTTACGTGTGACAGCAGAGAGGTACCTGTGTACAGAGGGCCCCAC 1032
|||||
Db 961 TCGTGTCCCGGGGTTTACGTGTGACAGCAGAGAGGTACCTGTGTACAGAGGGCCCCAC 1020
|||||
Oy 1033 CAGGTCCCTGGATGAGAGAGGCCCAAGCTCAGCTTACCTGCTGCCAAGCCACAGCTTGG 1092
|||||
Db 1021 CAGGTCCCTGGATGAGAGAGGCCCAAGCTCAGCTTACCTGCTGCCAAGCCACAGCTTGG 1080
|||||
Oy 1093 AAGAGAGATGTCCCTGTGTATATGTCAGAGCTGTCCCTCCGCGATACCTGCTGCCAA 1152
|||||
Db 1081 AAGAGAGATGTCCCTGTGTATATGTCAGAGCTGTCCCTCCGCGATACCTGCTGCCAA 1140
|||||
Oy 1153 CTCACGCTGGGGAGTGGGGGCTGCTGCCAATCCAGAGGCTGTGCTGCTGGACAC 1212
|||||
Db 1141 CTCACGCTGGGGAGTGGGGGCTGCTGCCAATCCAGAGGCTGTGCTGCTGGACAC 1200
|||||
Oy 1213 CAGCACTGCTGCCCCAGAGGATACAGTGTGTGTGAGGGGCAAGTGTACAGCAGAGAAC 1272
|||||
Db 1201 CAGCACTGCTGCCCCAGAGGCTACAGTGTGTGTGAGGGGCAAGTGTACAGCAGAGAAC 1260
|||||
Oy 1273 GAGATGCTGGGCTGAGTGGAGAGATGCTGCCGCCGCCGGCTTCCTTATCCACCCACA 1332
|||||
Db 1261 GAGATGCTGGGCTGAGTGGAGAGATGCTGCCGCCGCCGGCTTCCTTATCCACCCACA 1320
|||||
Oy 1333 GACATGCTGTGTACAGCAGACACAGCTGCCGCTGGGGGGAACCTGTGCTGCCAGCCAG 1392
|||||
Db 1321 GACATGCTGTGTACAGCAGACACAGCTGCCGCTGGGGGGAACCTGTGCTGCCAGCCAG 1380
|||||
Oy 1393 GGTGGGAGCTGGGGCTGTGCTGCCAGTGTGCCCATGTGTGTGTGCTGCGAAGATGCCAGAC 1452
|||||
Db 1381 GGTGGGAGCTGGGGCTGTGCTGCCAGTGTGCCCATGTGTGTGTGCTGCGAAGATGCCAGAC 1440
|||||
Oy 1453 TGGTGGCCGAGTGTACAGCTGCAAGTGAAGGCTGATCTGCGAGAGAGAGTGGTGC 1512
|||||
Db 1441 TGGTGGCCGAGTGTGTACAGCTGCAAGTGAAGGCTGATCTGCGAGAGAGAGTGGTGC 1500
|||||
Oy 1513 TGTGCCAGGCTGCACTTCTCTGAGCCGCTGAGCCCTCAGCTGGGTGTGAAGAGAGTGGAG 1572
|||||
Db 1501 TGTGCCAGGCTGCACTTCTCTGAGCCGCTGAGCCCTCAGCTGGGTGTGAAGAGAGTGGAG 1560
|||||
Oy 1573 TGTGGGAGAGGACATTTCTGCAATGATACCAACCTGCTGCGAGAGCAACCGAGGGC 1632
|||||

Db 1561 TGTGGGAGAGGACATTTCTGCCATGATTAACAGACCTGCTGCCAGAGCAACCGAGGGC 1620
Oy 1633 TGGGCTGTGCTGCTCCACAGCCAGGGGCTGTGTGTGTGATGAGGGCCACTGCTGCT 1692
Db 1621 TGGGCTGTGCTGCTCCACAGCCAGGGGCTGTGTGTGTGATGAGGGCCACTGCTGCT 1680
Oy 1693 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1752
Db 1681 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
Oy 1753 GAGGCCCCCTTGGAGGAGCCAGGCTTGAAGACCTGCTG 1791
Db 1741 GAGGCCCCCTTGGAGGAGCCAGGCTTGAAGACCTGCTG 1779
|||||
RESULT 6
US-08-991-862-1
; Sequence 1, Application US/08991862
; Patent No. 6309826
; GENERAL INFORMATION:
; APPLICANT: Serrero, GINETTE
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996 488/P001-A
; CURRENT APPLICATION NUMBER: US/08/991,862
; EARLIER FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 89/863,862
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2137
; TYPE: DNA
; ORGANISM: Mouse epithelin/granulin
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (23)..(1789)
; OTHER INFORMATION: The sequence is identical to that of the published
; OTHER INFORMATION: mouse granulin except for one nucleotide (T
; OTHER INFORMATION: instead of G) at position 1071 of gp88 cDNA
; OTHER INFORMATION: (position 1056 of mouse granulin).
US-08-991-862-1
Query Match 57.3%; Score 1200; DB 4; Length 2137;
Best Local Similarity 75.6%; Pred. No. 8e-292;
Matches 1572; Conservative 0; Mismatches 485; Indels 21; Gaps 6;
Oy 1 CGCAGCAGACATGTGAGACCTGTGAGCTGGGTGCTTAAACAGCAGGGCTGTGCT 60
Db 11 CGCAGCAGACATGTGAGAGCTGTGAGCTGGGTGCTTAAACAGCAGGGCTGTGAGCC 70
Oy 61 GGAACGGGTGGCCAGATGTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 71 GGAACAGAGTGTCCAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 130
Oy 121 GCCAGCTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 131 GCCAATCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 190
Oy 181 CTGGGGCCCCCGCCAGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 191 CTGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 250
Oy 241 GTCTCAGAGGACTTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 251 GTGTGTGAGCTTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 310
Oy 301 CACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 311 CACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 370
Oy 361 GGTAAACATCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 371 G--ATTAACCCCTTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 427
|||||

Db	658	TGCTGAGGCTACCACTGGGAGGATGAGGTGGTTCGAATGCCAACGCCATCTGCTGT	71.7
Qy	733	TCGCATACCTGCACACTGCTGCCCCCAAGACACTGTGTGTGACCTGATCCAGATGAATGC	79.2
Db	718	TCGCACCACTGCACACTGCTGCCCCCAAGACACTGTGTGTGACCTGATCCAGCAAGTGC	77.7
Qy	793	CTCTCAAGAGAAACGCTGACACGAGACCTCTCACTAACTCCCTGCGCAGACACATGGGC	85.2
Db	778	ATATCCAGAAGACATAC---ACCAAGATCTCATGACCAAGCTCCCTGATACCAAGTGAAT	83.4
Qy	853	GATGTGAATATGTGACATGAGGTGAGCTGCCCCAGATGCGTATACCTGCTGCCGTACAG	91.2
Db	835	GAGGTGAAGATGCGCACTTGAGGTGAGCTGCTCCGATGAGCTACACCTGCTGCCGCTTAAC	89.4
Qy	913	TCGGGGGCGCTGGGGCTGCTCCCTTTTACCAGGGCTGTGCTGTGAGAGACACATTAAC	97.2
Db	895	ACTGGGGCTGGGGCTGCTGCTCCATTCACCAAGGCTGTGTGTGTGAAGACCACTTAAC	95.4
Qy	973	TGCTGTCCGCGGGGTTTACGTGTGACACGACGAAAGGTAACCTGTGAACAGGGGCCAC	103.2
Db	955	TGCTGCCACGCGGGTTTCAGTGTCAACAGAGACAGAACTGTGAAGTGGAGTCTCTT	101.4
Qy	1033	CAGGTGCCCTGATGAGAAAGGCCCAAGCTCACTAGCTGCGCAGACCCACAACTTG	109.2
Db	1015	CAGGTACCTGTGATGAAAAAGGTCACGGGCTCCCTAGGCTCCAGACCCACATGTTTG	107.4
Qy	1093	AAGAGATGTCCCTGTGATATGTACAGAGCTGTCCCTCCGATACCTGCTGCCAA	115.2
Db	1075	AAGAAATATGTCCCTGTGATATGTACAGAGCTGTCCCTCCGATACCTGCTGCCAA	113.4
Qy	1153	CTCAGTCTGGGGAGTGGGGCTGCTGTCCAACTCCAGAGGCTGTGCTGCTGGACAC	121.2
Db	1135	CTCAGTCTGGGGAGTGGGGCTGCTGTCCAACTCCAGAGGCTGTGCTGCTGCTTAACAC	119.4
Qy	1213	CAGACATGCGCCCCCGACATACAGGTGTGATGCGGAGGGCAGTGTGAGGAGGAAG	127.2
Db	1195	CAGCATGTCTGCGGACATGGGGCTGCTGTCCAACTCCAGAGGCTGTGCTGCTTAACAC	125.4
Qy	1273	GAGATCTGGCTGTGACTGAGAAAGATGCTTGCCTGCCCGCGGGTTCCTTATCCACCCAGA	133.2
Db	1255	AGAAATGTGTGCTGTGGCTGTGGAGAAATGCTTGCCTGCCCGACAACTGTGCTCCAACTGGA	131.4
Qy	1333	GACATGGGCTGTACACACGACACCACTGTCCGGGTGGGGGAACCTGCTGCCGAGCCAG	139.2
Db	1315	GATATGTGTGTGACACGCACTACCACTGTGCCAGTAGAGGCAAACTGTGCCCAAGCTGT	137.4
Qy	1393	GGTGGAGAGCTGGGGCTGCTGTCCAGATTGGCCCAATGCTGTGTGCGAGAGATGCCACAC	145.2
Db	1375	AAGGGAAGTTGGGGCTGCTGTCCAGATTGGCCCAATGCTGTGTGTGAGAGACCGGACAC	143.4
Qy	1453	TGCTGCCCGGTGTGACTACACCTTCCAACTGTGAAGGTCGATCTGTGCGAGAAAGTAAGTGT	151.2
Db	1435	TGTTGCCCGGTGTGTGACTACACCTTCCAACTGTGAAGGTCGATGTGAAGAAAGATCAAGC	149.4
Qy	1513	TCCTGCCAGGCTGTGACACTTCCAGGGCCGAGCCCTCAGCTGGGTGTGAAGAGCTGGAG	157.2
Db	1495	TCCTTCCAGGCTTTCATGAGACCTGACCTTTGGCTCTAAAGTTGG-----GAACTGGA	154.8
Qy	1573	TGTGGGGAAGGAACTTCTTCCATGATTAACACAGACTGTGCCGAGAACCCGACAGGCG	163.2
Db	1549	TGTGTGTCCCGGACATTTCTGCAATGATTAACAGACTCTGTTGTGAAGACGCAAGGAAGC	160.8
Qy	1633	TGGGGCTGCTGTCCCTACGCCCCAGGGCGTGTGTGTGCTGATCGGCGCACTGCTGTCT	169.2
Db	1609	TGGGGCTGCTGTCCCTATGTAAAGGGTGTCTGTGTGAAGATGAGAGTCACTGTGTCTC	166.8
Qy	1693	GCTGCTCTCGCTGCGACACGAGGGGTACCAAGTGTTCGCGAGGAGGGCCCCGCGCTGG	175.2
Db	1669	ATGTGCTTCACTGTTTACGCCAAGGGACCAAGTGTTCGCGAAGAAAGCCCCCTGCTGG	172.8
Qy	1753	GAGCGCCCTTTGAGGAGCCAGCCTTGAGACAGCTGCTG	179.1

```

Db 1729 GACATCTTTGAGGATCCAGCCCAAGACCGTACTG 1767

RESULT 11
US-07-668-648-5
: Sequence 5, Application US/07668648
: Patent No. 5416192
: GENERAL INFORMATION:
: APPLICANT: Shoyab, Mohammed
: APPLICANT: Plozman, Gregory D.
: TITLE OF INVENTION: EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH
: TITLE OF INVENTION: MODULATING PROTEINS
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/668,648
: FILING DATE: 19910819
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Mistrock, S. Leslie
: REGISTRATION NUMBER: 18,872
: REFERENCE/DOCKET NUMBER: 5624-161-999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212)790-9090
: TELEFAX: (212) 869-9741
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1767 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: ORIGINAL SOURCE:
: ORGANISM: Mus musculus
: TISSUE TYPE: Kidney
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1767
US-07-668-648-5

Query Match 52.9%; Score 1107.4; DB 1; Length 1767;
Best Local Similarity 77.6%; Pred. No. 1.3e-266;
Matches 1381; Conservative 0; Mismatches 386; Indels 12; Gaps 3;

QY 13 ATGTGACCCCTGCTGAGTGGGTGGCTTTAACAGAGGGCTGTGGTGGAAACGGGTGC 72
Db 1 ATGTGGGTCCTGATAGCTGTGGCTGGCTTCGCGGAGGGCTGTAGCGGAACACAGTGT 60

QY 73 CCAGATGCTCAGTTGTGCGCTGTGGCTGTGCTGTGACCCCGGAGGAGCCAGCTACAGC 132
Db 61 CCAAGTATGGGACGTTGTGGCTCTTTGCTGTGCTGTGACGAGGAGGAGCCACACTACAGC 120

QY 133 TGCTGCGCTCCCTCTTCTGTGAGCAATATGCGCCACACACACTGAGCAGGACTCTGGGTGGCCCC 192
Db 121 TGCTTTAACCTCTTCTGTGAGCAATATGAGGCTAGAAATTAAGAGCCATCATCTAGATGGCTCC 180

QY 193 TGCCAGGTGATATGCCCATGCTGTGCGCGGCACTCTGCATCTTAACGCTGCAGAGGACT 252
Db 181 TGCCAGACCCATGCGCACTGTCTGTGCTGTGCTGTATTTCTTGTCTTCTACGTGTGTGGACT 240

QY 253 TCCAGTCTTGCGCCCTTCCACAGAGCGGTGGCATCGGGGATGGCCATCACTGTGCCCA 312

```

Db 241 TCACGCTCTGCTGCTCTCTAAGGGTGTGTCTTGTGTGATGCTTACCACTGTGCCCC 300
Qy 313 CGGGGCTTTCACATGCAATGAGACAGCGGAGATCTGCTTCCAAAGATCAAGTAACTCC 372
Db 301 CAGGGCTTTCACATGCAATGAGATGGAATGCTCTTCCAAAGATCAAGTAACTCC 357
Qy 373 GTGGGTGCTTTCACATGCAATGAGATGGAATGCTCTTCCAAAGATCAAGTAACTCC 432
Db 358 GTGGGTGCTTTCACATGCAATGAGATGGAATGCTCTTCCAAAGATCAAGTAACTCC 417
Qy 433 GTTATGCTGATGCTTCCGAGGAGTGTGCTTCCGAGGAGTGTGCTTCCGAGGAGTGTG 492
Db 418 ATTATGCTGATGCTTCCGAGGAGTGTGCTTCCGAGGAGTGTGCTTCCGAGGAGTGTG 477
Qy 493 AGGGTGCATGCTTCCGAGGAGTGTGCTTCCGAGGAGTGTGCTTCCGAGGAGTGTG 552
Db 478 AGAGTGCATGCTTCCGAGGAGTGTGCTTCCGAGGAGTGTGCTTCCGAGGAGTGTG 537
Qy 553 CCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 612
Db 538 CCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 597
Qy 613 GCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 672
Db 598 TCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 657
Qy 673 TGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 732
Db 658 TGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717
Qy 733 TCCGATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792
Db 718 TCCGATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 777
Qy 793 CTCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 852
Db 778 CTCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 834
Qy 853 GATGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 912
Db 835 GATGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 894
Qy 913 TCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 972
Db 895 ACTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 954
Qy 973 TGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1032
Db 955 TGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1014
Qy 1033 CAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1092
Db 1015 CAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1074
Qy 1093 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1152
Db 1075 AAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1134
Qy 1153 CTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1212
Db 1135 CTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1194
Qy 1213 CAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
Db 1195 CAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1254
Qy 1273 GAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1332
Db 1255 ACAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1314
Qy 1333 GACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1392
Db 1315 GATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1374

Qy 1393 GGTGGAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1452
Db 1375 AAGGAGATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1434
Qy 1453 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1512
Db 1435 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1494
Qy 1513 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1572
Db 1495 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1548
Qy 1573 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1632
Db 1549 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1608
Qy 1633 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1692
Db 1609 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1668
Qy 1693 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1752
Db 1669 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1728
Qy 1753 GACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1791
Db 1729 GACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1767

RESULT 12

US-08-429-998-5

Sequence 5, Application US/08429998

Patent No. 5885961

GENERAL INFORMATION:

APPLICANT: Shoyab, Mohammed

APPLICANT: Flowman, Gregory D.

TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH

TITLE OF INVENTION: MODULATING PROTEINS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/429, 998

FILING DATE: 27-Apr-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/668, 648

FILING DATE: 13-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Mirock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 5624-161-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)790-9090

TELEFAX: (212) 869-9741

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1767 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

ORIGINAL SOURCE:
ORGANISM: Mus musculus
TISSUE TYPE: Kidney
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1767
US-08-429-998-5

Query Match 52.9%; Score 1107.4; DB 2; Length 1767;
Best Local Similarity 77.6%; Pred. No. 1.3e-268;
Matches 1381; Conservative 0; Mismatches 386; Indels 12; Gaps 3;

13 ATGTGACCTGGTGAAGCTGGGCTTAAACAGCAGCGCTGGCTGGAAGCGGCTGC 72
1 ATGTGGGCTCTGATGAGTGGCTGGCTTGGCGAGGGCTGGAGCGGGAACAACATGT 60
73 CAGATGATGATGCTGGCCCTGGGCTGTGCTGGAGCCCGGAGGAGGACAGTACAGC 132
61 CAGATGAGGAGTGTGGCTGGCTGGCTGGCTGGCTGGAGCAGGAGGAGGAGGAGGAG 120
133 TGTGCTGCTGCTGGCTGGAGCAATGAGCCCAACACTGAGCAGGAGCTGGGAGCCGC 192
121 TGTGTAACCTCTTCTGGAGACATGGCCTAGATAAGAGCCATCATAGATGGCTCC 180
193 TGTGAGGTGATGAGCCAGCTGCTGGCGGCACTCTGCAATCTTTACGCTCAGGAGCT 252
181 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
253 TGTGAGTGTGCTGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 312
241 TGTGAGTGTGCTGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
313 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 372
301 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 357
373 GGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 432
358 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417
433 GGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 492
418 ATGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 477
493 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 552
478 AGAGTGTGATGCTGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 537
553 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 612
538 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 597
613 GGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 672
598 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 657
673 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 732
658 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 717
733 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 792
718 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 777
793 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 852
778 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 834
853 GATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 912
835 GAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 894
913 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 972

895 ACTGGGGGCTGGGGCTGCTCTCCATTTTCCAGAGGCCGTGTGTGTGAGATACATTCAT 954
973 TGTGATCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1032
955 TGTGATCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1014
1033 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1092
1015 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1074
1093 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1152
1075 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1134
1153 CTCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1212
1135 CTCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1194
1213 CAGCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1272
1195 CAGCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1254
1273 GAGATGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1332
1255 ACAATGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1314
1333 GACATGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1392
1315 GATATGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1374
1393 GGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1452
1375 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1434
1453 TGTGATCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1512
1435 TGTGATCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1494
1513 TGTGATCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1572
1495 TGTATCCAGGCTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1548
1573 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1632
1549 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1608
1633 TGTGATCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1692
1609 TGTGATCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1668
1693 GGTGATCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1752
1669 GGTGATCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1728
1753 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1791
1729 GACATGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1767

RESULT 13
US-08-431-333-5
Sequence 5, Application US/08431333
Patent No. 5965723
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plozman, Gregory D.
TITLE OF INVENTION: NOVEL CYSTEINE-RICH GROWTH
NUMBER OF SEQUENCES: 12
MODULATING PROTEINS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 21, 2003, 12:51:09 ; Search time 2706 Seconds
(without alignments)
12538.634 Million cell updates/sec

Title: US-08-991-862-16
2095
Perfect score: 1 cgcgcagcagacatgttgac.....ataaagttgtcacttctt 2095
Sequence:

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mem:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1209.6	57.7	2145	11	AK013678 Mus muscu
2	1208	57.7	2170	11	AK018744 Mus muscu
3	966.2	46.1	986	9	AL548072 AL548072
4	949.2	45.3	1089	13	BM54590 AGENCOURT
5	943.6	45.0	1033	9	AL551350 AL551350
6	928.4	44.3	1010	9	AL542702 AL542702

c	7	918	43.8	1018	9	AL572883	AL572883
c	8	914	43.2	932	9	AL561424	AL561424
c	9	904	43.6	996	9	AL582634	AL582634
c	10	901.8	43.0	934	9	AL541798	AL541798
c	11	880.6	42.0	920	9	AL552664	AL552664
c	12	873.8	41.7	942	9	AL542659	AL542659
c	13	870.4	41.5	894	9	AL557765	AL557765
c	14	854.4	40.8	888	9	AL544054	AL544054
c	15	849	40.5	991	13	BM468251	BM468251
c	16	848.6	40.5	919	14	B0878155	B0878155
c	17	843.8	40.3	930	14	B0681528	B0681528
c	18	841.8	40.2	1004	14	BM07165	BM07165
c	19	837.6	40.0	950	14	B036810	B036810
c	20	834.2	39.8	1126	13	BM544984	BM544984
c	21	832.4	39.7	979	14	BM19561	BM19561
c	22	831	39.7	928	14	B0683772	B0683772
c	23	828.2	39.5	881	14	B018213	B018213
c	24	822.6	39.3	1035	14	B0061031	B0061031
c	25	821.6	39.2	995	14	B0706302	B0706302
c	26	820.6	39.2	865	9	AL551474	AL551474
c	27	819.8	39.1	936	14	B0925345	B0925345
c	28	819.2	39.1	924	14	B0706910	B0706910
c	29	819.2	39.1	1126	13	BM550274	BM550274
c	30	817.8	39.0	900	9	AL574944	AL574944
c	31	816.8	39.0	1062	14	BM808271	BM808271
c	32	815.6	38.9	865	9	AL554194	AL554194
c	33	813.4	38.8	855	13	BM009189	BM009189
c	34	812	38.8	895	14	B0900375	B0900375
c	35	811	38.7	1033	14	B058416	B058416
c	36	810.8	38.7	1004	13	BM562443	BM562443
c	37	807.4	38.5	948	14	B0958748	B0958748
c	38	806	38.5	923	14	B0650063	B0650063
c	39	804.8	38.4	929	14	B0955902	B0955902
c	40	804.8	38.4	975	14	B0960488	B0960488
c	41	804.8	38.4	1047	14	B052452	B052452
c	42	803.2	38.3	938	14	B0920068	B0920068
c	43	801.8	38.3	1007	14	B0060872	B0060872
c	44	800.8	38.2	1026	13	BM554117	BM554117
c	45	799.2	38.1	1031	14	B0061852	B0061852

ALIGNMENTS

RESULT 1	AK013678
LOCUS	AK013678
DEFINITION	Mus musculus adult male hippocampus cDNA, RIKEN full-length
ACCESSION	AK013678
VERSION	AK013678.1 GI:12651131
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (strain:c57BL/6J) adult male hippocampus cDNA to mRNA, clone:2900053623.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
AUTHORS	Preparation and subtraction of cap-trapper-selected cDNAs to
TITLE	Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL	20499374
MEDLINE	11042159
PUBMED	3
REFERENCE	

AUTHORS
Shibata, K., Itoh, M., Atzawa, K., Nagaoka, S., Sasaki, N., Carninci, P.
Konno, H., Akiyama, J., Nishl, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaiguchi, S., Ikegami, Y., Kasaihiagi, K.,
Fujimake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawal, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
TITLE
RIKEN integrated sequence analysis (RISA) system—384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL
Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE
20530913
PUBMED
11076861
REFERENCE
4
AUTHORS
Kawal, J., Shinaagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,

TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21085660
PUBMED	11217851
REFERENCE	5 (pages 1 to 2145)
AUTHORS	Adachi, J., Aizawa, K., Akahira, S., Akinura, T., Mono, H., Arai, A.,

TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physiological and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Fax: 81-45-503-9216)
COMMENT Please visit our web site (<http://genome.gsc.riken.go.jp/>) for

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGGAGAGAGAGATCCAAAGGAGCTCTTTTTTTTTTTTAAVN 3'], cDNA was prepared by using tetralox thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGGAGAGAGATTCGAGCTATTATTAATTAATCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR.

FEATURES

source

```

1..2145
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:2900053G23"
/db_xref="MGI:1896279"
/db_xref="taxon:10090"
/clone="2900053G23"
/sex="male"
/tissue_type="hippocampus"
/clone_id="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1..2145
/gene="Grn"
43..1812
/gene="Grn"
/note="data source:MGI, source key:MGI:95832, evidence:ISS
granulin
putative"
/codon_start=1
/protein_id="BAB28951.1"
/db_xref="GI:12851132"
/db_xref="MGD:MGI:95832"
/translational="MMYLMISLAFAGLVATGTGTCGGPQSGCPVACCLIDOGGANSCNP
LIDTPRITSHHLDGSCOTPHGMHPCAGTSCILYSCTSSCCPFSEKGVCSGGYHYHCPRG
PHSADKSCFPMSDNPLIAGVOCCPSGFPEPDASATCTIMDGSMGCCPMFOASCEDR
VHCCPHGASCDLVHTRCVSPGTHTLTKRPAACTNVAVALPSVVCDAKTQCDDSDS
TCCELPTGKYGCCEPMNAICCSDLHCCPODVCDLIQSCLSKNTYDILLTKLPGYR
VKLEIKCMDEVSECEGYTCRLNTGAMGCCPFAPAVCEDHIHCCPAFGCHTEKGCE
MKLIQVPMKKVIAPLRLLPDPOLIKSTPDDEFRCPTNNCKINSGDGCCPIEPA
VCSDSNHCCPGOFTCIAGCGCKGDMVAGLKIPAROTPLQIDIGCDQHTSCV
GQVCCBSLGKSMACCQLPRAVCCEDRHCCPACTCNVAKRTCKVDYLQPLVLTL
GPVGNVECEGEHFCHDNQFCCKDSAGVMACPYLKGVCCRDRHCCPGSFHSARGT
KCRLRK.IPRMDMLRBPVRPL"
2126..2131
/gene="Grn"
/note="putative"
polyA_signal
2145
/gene="Grn"
/note="putative"
polyA_site
BASE COUNT      436 a      619 c      586 g      504 t
ORIGIN
Query Match      57.7%; Score 1209.6; DB 11; Length 2145;
Best Local Similarity 75.9%; Pred. No. 7.9e-281;
Matches 1578; Conservative 0; Mismatches 479; Indels 21; Gaps 6;
```

ID	Sequence	Score	DB	Length
QY	1 CGCACGGACGACCATGTGACACCGCTGTAGACGGGGTGCGCTTAACAGCAGGCGCTGTGGCT	60		
Db	31 CGCACGGACGACCATGTGCGCTCTGATGACGGGGCTTGCGGCGACGGCGCTGTACCC	90		
QY	61 GAACACGGGTCGCCAGATGTGTCACTTTCGCCCTGTGGCTCTCTCCCTGGACCCGGAGAGA	120		
Db	91 GGAAACACAGTGTCCAGATGGGACATTCTGCCCCCTGTGTGCTCTGCTTGAACAGGAGGA	150		
QY	121 GCCACGTACACAGCTCTGCCGCTGCCCTTCTGTGACAATAATGGCCCACACACTGACGAGCAT	180		
Db	151 GCCAACCTACAGCTCTGTAAACCCCTCTCTGTGACACATGGCTAGAAATTAACAGACCAT	210		
QY	181 CTGGGGTGGCCCCCTGCGACAGTTGATGATGCCACATGCTCTGCGGGCACCTCTGCATCTTTACC	240		
Db	211 CTAATATGGCTCTTCCAGACCCATAGGCGCACTGCTGTGGCTATTTCTTGTCTTCTACAT	270		
QY	241 GTCTCAGGAGACTTCAGATGTCTGCCCTTCCACAGAGGCGGTGACATGGGGATGGGCAT	300		
Db	271 GTGTCTGGGACTTCCAGCTGCTGCCCTTCTCTTAAGGCTGTGTCTTGTGTGATGGCTAC	330		
QY	301 CACTGTGCCCCACGGGGCTTTCACCTGCAGTGCAGACAGGGGCATCTGCTTCCAAGATCA	360		
Db	331 CACTGTGCCCCACGGGGCTTTCACCTGTAGTGTACATGGGAATCTCTGCTTCCAATGTCA	390		
QY	361 GGTAAACAATCTCGTGGGTGCATCCAGTGCCTGTATGTACTGATTCGAATGCCCGGACTTC	420		

Db 391 G---ATTAACCCCTTGGGTCTGTCAGTCTCCGGAGGACGATTTAAATGCTCTGACTCT 447
 Oy 421 TCCAGTGTCTGTATGTGATGATGCTCTGAGGGTGTGCCCCATGCCCCAGGCTTC 480
 Db 448 GCCACTGCTGCTATGTGATGATGCTCTGAGGGTGTGCCCCATGCCCCAGGCTTC 507
 Oy 481 TGTGTGAAGACAGGGTGTGATGCTCTGAGGGTGTGCCCCATGCCCCAGGCTTC 540
 Db 508 TGTGTGAAGACAGGGTGTGATGCTCTGAGGGTGTGCCCCATGCCCCAGGCTTC 567
 Oy 541 CCGTGTATACACCCACGAGGACCCACCCCTGAGGAAAGAGTCTCCCTGAGGAGACT 600
 Db 568 CGATGGTGTACCCACGAGGACCCACCCCTGAGGAAAGAGTCTCCCTGAGGAGACT 627
 Oy 601 AACAGGACAGTGTCTGTGTCAGTCTGATGCTGAGGAGGAGGAGGAGGAGGAGGAG 660
 Db 628 AACAGGACAGTGTCTGTGTCAGTCTGATGCTGAGGAGGAGGAGGAGGAGGAGGAG 687
 Oy 661 GATGTTTCTACTGCTGTGAGTGTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
 Db 688 GATGTTTCTACTGCTGTGAGTGTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 747
 Oy 721 GCCACTGCTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
 Db 748 GCCACTGCTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 807
 Oy 781 CAGAGTAAAGTGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 Db 808 CAGAGTAAAGTGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 864
 Oy 841 CACACATGGGCGATGTAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
 Db 865 TACCCATGTAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 924
 Oy 901 TGCCTGTACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
 Db 925 TGCCTGTACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 984
 Oy 961 GACACATGTAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
 Db 985 GATCATTGTAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1044
 Oy 1021 CAGGGGCCCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
 Db 1045 ATGCGATCTCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1104
 Oy 1081 CCACAAGCCCTGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
 Db 1105 CCACAAGCCCTGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1164
 Oy 1141 ACCTGTGCTCACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
 Db 1165 ACCTGTGCTCACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1224
 Oy 1201 TGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
 Db 1225 TGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1284
 Oy 1261 CAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
 Db 1285 CAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1344
 Oy 1321 TCCACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
 Db 1345 CTCCTCAATTTGAGATATCGGTTGTGACACACATATCCAGGAGGAGGAGGAGGAGGAGGAG 1404
 Oy 1381 TGCCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
 Db 1405 TGCCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1464
 Oy 1441 GATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500

Db 1465 GACCGGACGACGATGTGCCCCGGGGGTACACCTGCATGTGAAGGAGGAGGAGGAGGAGGAG 1524
 Oy 1501 AAGGAAGTGTCTCTGCGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
 Db 1525 AAGGATGTGATTTTATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1580
 Oy 1561 AAGGATGTGATTTTATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1620
 Db 1581 --GATGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1638
 Oy 1621 AACCGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
 Db 1639 AGTGCAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1698
 Oy 1681 CACTGTGTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1740
 Db 1699 CACTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1758
 Oy 1741 GCCCGGCGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800
 Db 1759 ATTCTGTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1818
 Oy 1801 GTACTGAA-----GACTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1853
 Db 1819 GCTACAGACTTAAAGAACTCCACAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1878
 Oy 1854 AGGCTGTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1912
 Db 1879 AGGCTGTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1938
 Oy 1913 ATCACATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1971
 Db 1939 ATCACATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1998
 Oy 1972 CAAAAGCCCAATTAACAGCTGCATCCCTCCCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2031
 Db 1999 CAAAAGCCCAATTAACAGCTGCATCCCTCCCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2058
 Oy 2032 TTTTCCCTATCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2069
 Db 2059 TCTTCCGAG 2096

 RESULT 2
 AK018744
 LOCUS
 DEFINITION
 Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610012H06:granulin, full insert sequence.
 ACCESSION
 AK018744.1
 VERSION
 AK018744.1
 KEYWORDS
 HTC; CAP trapper.
 SOURCE
 Mus musculus (strain:C57BL/6J) adult male kidney cDNA to mRNA, clone:lib:RIKEN full-length enriched mouse cDNA library
 clone:0610012H06.
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 JOURNAL
 MEDLINE
 PUBMED
 99279253
 10349636
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 JOURNAL
 MEDLINE
 PUBMED
 20499374
 11042159
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

TITLE	JOURNAL	PUBMED	REFERENCE
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer	Genome Res.	10 (11), 1757-1771 (2000)	
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaueuchi, S., Ikegami, T., Kashiwagi, K., Fujiyake, S., Inoue, K., Togawa, Y., Iwawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kiru, A. and Hayashizaki, Y.			
Kawai, J., Shitagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,			4

TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21085660
PUBMED	11217851
REFERENCE	5 (bases 1 to 2170)
AUTHORS	Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,

REFERENCE	AUTHORS
5 (pages 120 to 2170)	
	Aaschi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Butt,C., Canicelli,P., Fukunoda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F., Hume,D., Imocani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawaji,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kuribara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Nunazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Schirml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sobabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I., Yanagishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
	Direct Submission
	Submitted (18-AUG-2000) yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.go.jp, URL: http://genome.gsc.riken.go.jp/ , Fax:81-45-503-9216)
	Please visit our web site (http://genome.gsc.riken.go.jp/) for
COMMENT	

further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5', GAGCAGAGACCGCCGCCACACTCGAGTTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went by through one round of normalization to Seq = 5.0. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGCAGAGAGAGATCCAGACGCTCATTTATTTATTTAAACCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end; SstI; 3' end; XhoI. Host: *Shorl*.

FEATURES		SOURCE	
1. .2170		Location/Qualifiers	
/organism="Mus musculus"			
/strain="C57BL/6J"			
/db_xref="FANTOM,DB:0610012H06"			
/db_xref="MGI:1900100"			
/db_xref="taxon:10090"			
/clone="0610012H06"			
/sex="male"			
/tissue_type="kidney"			
/clone_id="RIKEN full-length enriched mouse cDNA library"			
/dev_stage="adult"			
1. .2170			
/gene="Gri"			
68.1837			
/gene="Gri"			
/note="data source:MGI, source key:MGI:95832, evidence:ISS"			
granulin			
putative"			
/codon_start=1			
/protein_id="BAB31384.1"			
/db_xref="GI:12858616"			
/db_xref="MGI:95832"			
/translation="MWYIMSLAFRAAGLIVAGTQCPDGFVACCLDGGAGNSCPNPLDTPRITSHLDGSCQTHGSHCAPAGISCLTVSGTSCSPFSKGVGSGDGRYHCCPAGFHCADGSCFQMSDNPGLAVQCPGSPFECDSATTCIMWDSKCCPMPDASCEDETRVCCPHGASCDLVHTKRCVSPGTHTLLKRPAAQNTNRAVSLPFSVCPDPAKTQCPDPSVCECLPTGKYGCCPMPNAICCSIDLHCCPDQTVCDLIQSCLSKNTYDILTKLPGYPRVKEVCKDEMSVSCPEGYTCRLNTGAMCCPFAKAVCCEDHICCPAGFOCHTEGTCSEMGILVPMWKVIAPLRLPDQILKSPDPPDPRCPNTNCCKLSNGSDMCCPIPEAVCSGDHOCGSGPQFTCAOCYCKGCKPMVAGLIEIIPARQTPAQIDGICDQHNKSPVGPQCTPSLKSGSMACQQLPHAVCCEDRPHCCPAGTICVAKARTCKEDVDFIOPVLLTLGPTKGVNCEGEGHFCNDNQTCCKDSAGVMACCPYLKGVCCRDHNCBPGFHCASRGTKCLKKKIPCDMFLRDPVPL"			
polyA_signal			
/gene="Gri"			
2151.2156			
/note="putative"			
polyA_site			
2170			
/gene="Gri"			
/note="putative"			
BASE COUNT		441 a 627 c 593 g 509 t	
ORIGIN			
Query Match		57.7%; Score 1208; DB 11; Length 2170;	
Best Local Similarity		75.9%; Pred. No. 1.9e-280;	
Matches 1577; Conservative		0; Mismatches 480; Indels 21; Gaps 6;	
QY	1	CGCAGGCGACACATGTGACACCTGTGTGAGCTGGGTGGCGCTTAACAGCAGGCGTGTGGCT	60
DB	56	CGCAGGCGACACATGTGGGTCTGTATGAGCTGGCGCTTTCGCGGCGAGGCTGTGTAACT	115
QY	61	GAAAGCGCGGTGCCGAGATGATGATGATGACCTGTGGCGCTGTGTGCTGTGACCCCGAGAGA	120
DB	116	GGAACACAGTGTCCAGATGGGCAAGTTCGCTGTGGCTGTGCTGTGACCGAGGAGGA	175
QY	121	GCCAGCTACAGCTGTGCGCTGCCCTTCTGTGCAAAATGGCCCAACAACACTGACGAGCAT	180
DB	176	GCCAACTACAGCTGTGTAAACCCCTTCTGTGACACATGACCTAGAAATAAAGACATCAT	235
QY	181	CTGGGTGGCCCCCTGCGACAGTGTGATGATGCCACATGCTCTGTGCGCGGCACTCTCGATCTTTAC	240
DB	236	CTAGATGGCTCTGTGCAACCCATGGCCACATGCTCTGTGCTATCTTCTTCTCTACT	295
QY	241	GTCCTAGGAGCTTCACATGTGTGCTGCCCTTCCACAGAGCGGTGGCATTTGGGGGATGGCAT	300
DB	296	GTGTCTGGGACTTCCAGCTGCTGCTGCCCTTCTTAAAGGTGTGTCTTGTGTGATGGCTTAC	355
QY	301	CACGTCTCCCAAGCGGGCTTCACATGCACTGCACTGACAGAGCGGCGATCTCTCCAAAGATCA	360
DB	356	CACGTCTCCCAAGCGGGCTTCACATGCACTGCACTGACAGATGGGAAATCTGCTTCCAGATGCA	415
QY	361	GGTAAACAATCCGTTGGGTGCATTCAGTGGCCCTGTATGATGATGCAATGCCCGGACTTC	420

Db 416 G---AATACCCCTTGGGTCTGTCTGACAGTCTCCGGGAGCCAGTTTAATGTCTGTGACTCT 472
OY 421 TCCAGTGGCTGTGTATGGTATGATGCTCTGTGGGGGAGTCCGACATGACGAGGTTCC 480
Db 473 GCCACCTGCTGCAATTAATGTTGATGTTGTTGGGATGTTTCCATGCCCAAGGCTCT 532
OY 481 TGGTGTGAAGACAGAGGTGACAGTCTGTCCGACAGTGTCTTTCGACAGCTGTTCACAC 540
Db 533 TGGTGTGAAGACAGAGTGTGATGCTTCCCATGGGGCTCTGTGATCCGTGTTCACACA 592
OY 541 CGGTGATACACCCACAGGAGCCACCCCTGTGGCAAGAGTCTCTCCCTCCAGAGACT 600
Db 593 CGATGGTTTACCCACAGGAGCCACACCTCTAAGAGTCTCTCCCTGACAAAAGACC 652
OY 601 AACAGGAGAGTGGCTGTGTCAGAGTGTGTCTCCGAGGAGGAGGAGGAGGAGGAGGAG 660
Db 653 AACAGGAGAGTGTGTTTGTCTTCTTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 712
OY 661 GATGTTTACCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 720
Db 713 GATGATTTTACCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 772
OY 721 GGCACCTGT 780
Db 773 GGCATGT 832
OY 781 CAGAGT 840
Db 833 CAGAGT 889
OY 841 CACACAGT 900
Db 890 TACCCAGT 949
OY 901 TGGCTGT 960
Db 950 TGGCTGT 1009
OY 961 GACACATGT 1020
Db 1010 GATCAGATGT 1069
OY 1021 CAGGGGCCCCCAGAGT 1080
Db 1070 ATGAGT 1129
OY 1081 CCACAGT 1140
Db 1130 CCACAGT 1189
OY 1141 ACCTGT 1200
Db 1190 ACCTGT 1249
OY 1201 TGGT 1260
Db 1250 TGGT 1309
OY 1261 CAGCGAGGAGGAGT 1320
Db 1310 CAGAGGAGGAGGAGT 1369
OY 1321 TCCGACCCGAGAGT 1380
Db 1370 CTTCGAATTTGGAGATGT 1429
OY 1381 TGGCCGAGCCAGGAGT 1440
Db 1430 TGGCCGAGCCAGGAGT 1489
OY 1441 GATTCGACAGT 1500

Db 1490 GACCGGACGACATGTTGCCCGGGGTACACCTGTGAATGTGAAGGAGGAGGAGGAGGAG 1549
OY 1501 AAGGAAGT 1560
Db 1550 AAGGATGT 1605
OY 1561 AAGGAGT 1620
Db 1606 --CAATGTGAGT 1663
OY 1621 AACGAGAGGAGT 1680
Db 1664 AGTGCAGAGT 1723
OY 1681 CACTGT 1740
Db 1724 CACTGT 1783
OY 1741 GCCCGCGCTGGAGCGCCCTTTGAGGAGCCAGCCCTTGAGAGCTGTGTGTGTGTGTGT 1800
Db 1784 ATTCCTGT 1843
OY 1801 GTACTGA-----GACTGTGAGCCCTGTGGAGCCCACTGTGGAGGAGGAGGAGGAGGAG 1853
Db 1844 GTTACAGACTTGAAGAACTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1903
OY 1854 AGGCTTCCCTAGGACCTCCCTTACCAAAATTCCTCCGTGAGCCCACTGTGTGTGTGTGTGT 1912
Db 1904 AGGCTTCCCTAGGAGCTTCCCTTACCAAAATTCCTCCGTGAGCCCACTGTGTGTGTGTGT 1963
OY 1913 ATCAGCATGGAGT 1971
Db 1964 ATCAGCATGGAGT 2023
OY 1972 CAAGAGCCCTTACAGCTGT 2031
Db 2024 CAAGAGCCCTTACCAAAATTCCTCCGTGAGCCCACTGTGTGTGTGTGTGTGTGTGTGT 2083
OY 2032 TTTTCCCTATCAGAGGAGT 2069
Db 2084 TCTTCCGAGCCACAGT 2121

RESULT 3
AL548072 986 bp mRNA linear EST 16-FEB-2001
LOCUS AL548072 LFL_NFL006_PL2 Homo sapiens cDNA clone CS0D1034Y17 5
DEFINITION prime, mRNA sequence.
ACCESSION AL548072
VERSION AL548072.1 GI:12882738
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 986)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: secref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1..986
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1034Y17"
/clone_lib="LFL_NFL006_PL2"
/issue_type="placenta"
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and

Cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : filiang@lifetech.com URL : <http://fulllength.invitrogen.com>

BASE COUNT 168 a 323 c 290 g 203 t 2 others
ORIGIN

Query Match 46.1%; Score 966.2; DB 9; Length 986;
Best Local Similarity 99.6%; Pred. No. 2.9e-222;

Matches 977; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

1 CGCAGGACACCATGTGACCCCTGGTGAAGCTGGTGGCTTAAACAGACAGGGCTGGTGGCT 60
6 CGCAGGACACCATGTGACCCCTGGTGAAGCTGGTGGCTTAAACAGACAGGGCTGGTGGCT 65
61 GGAAGCGGCTGCGCCAGATGCTGATTTGCGCTTGGCTGCTGGTGAACCCCGAGAGA 120
66 GGAAGCGGCTGCGCCAGATGCTGATTTGCGCTTGGCTGCTGGTGAACCCCGAGAGA 125
121 GCGAGCTACAGTGGTGGCCCTGCTGGACAAATGGCCCAACACTGAGCAGGCAT 180
126 GCGAGCTACAGTGGTGGCCCTGCTGGACAAATGGCCCAACACTGAGCAGGCAT 185
181 CTGGGTGGCCCTGCGCAGGTGATGATGCCACTGCTGCGCCACTGCTGATCTTTTACC 240
186 CTGGGTGGCCCTGCGCAGGTGATGATGCCACTGCTGCGCCACTGCTGATCTTTTACC 245
241 GTCTAGAGGACTTCAAGTTGCTGCCCCCTTCCAGAGCCGCTGGCATGGCGGATGGCCAT 300
246 GTCTAGAGGACTTCAAGTTGCTGCCCCCTTCCAGAGCCGCTGGCATGGCGGATGGCCAT 305
301 CACTGCTGCGCCAGGGGCTTCCACTGACAGTGCAGAGCGGGCATCTGCTTCCAAAGATCA 360
306 CACTGCTGCGCCAGGGGCTTCCACTGACAGTGCAGAGCGGGCATCTGCTTCCAAAGATCA 365
361 GGTAAACAATCCGTTGGGTGTCATCCAGTGCCTGATAGTCACTGGAATGCGCGGACTTTC 420
366 GGTAAACAATCCGTTGGGTGTCATCCAGTGCCTGATAGTCACTGGAATGCGCGGACTTTC 425
421 TCCAGTGGTGGTATGTTGATGATGGCTTCTGGGGGTGCTGGCCCATGGCCAGGCTTTC 480
426 TCCAGTGGTGGTATGTTGATGATGGCTTCTGGGGGTGCTGGCCCATGGCCAGGCTTTC 485
481 TCCGTGAAGACAGGGTGCATGCTGTCGCGAGGCTGCTTTCGACCTGGTTCACACC 540
486 TCCGTGAAGACAGGGTGCATGCTGTCGCGAGGCTGCTTTCGACCTGGTTCACACC 545
541 CGCTGATACACCAACGCGGACCCCAACCCCTGCGAAGAGAGCTCCCTGCCAGAGACT 600
546 CGCTGATACACCAACGCGGACCCCAACCCCTGCGAAGAGAGCTCCCTGCCAGAGACT 605
601 AACAGGGACAGTGGCTTGTCCAGTGGTGCATGTCGCGAGGACGACGGCCGGTGGCTT 660
606 AACAGGGACAGTGGCTTGTCCAGTGGTGCATGTCGCGAGGACGACGGCCGGTGGCTT 665
661 GATGTTTACCTGCTGTCAGCTGCCAGTGGGAGATATGCTGTGGCCCAATGGCCCAAC 720
666 GATGTTTACCTGCTGTCAGCTGCCAGTGGGAGATATGCTGTGGCCCAATGGCCCAAC 725
721 GCGACCTGCTGCTCGATACCTGTCATGCTGCGCCCAAGACACTGTGTGTGACCTGATC 780
726 GCGACCTGCTGCTCGATACCTGTCATGCTGCGCCCAAGACACTGTGTGTGACCTGATC 785
781 CAGATTAAGTGGCTCTCCAGAGAGAACGCTTACACAGGACTCTCTACTTAAGTGGCTGGC 840
786 CAGATTAAGTGGCTCTCCAGAGAGAACGCTTACACAGGACTCTCTACTTAAGTGGCTGGC 845
841 CACACAGTGGGATGTGAATGTGACATGGAGTGAAGTGGCCAGATGGGCTATACCTGC 900
846 CACACAGTGGGATGTGAATGTGACATGGAGTGAAGTGGCCAGATGGGCTATACCTGC 905

QY 901 TGCCCTTACACTCGGGGGCCCTGGGCTGTCGCCCTTTTACCAGGCTGTGTGTGAG 960
DB 906 TGCCCTTACACTCGGGGGCCCTGGGCTGTCGCCCTTTTACCAGGCTGTGTGTGAG 965
QY 961 GACCAATACACTGCTGTGCC 981
DB 966 GACCAATACACTGCTGTGCC 985

RESULT 4
BM554590 1089 bp mRNA linear EST 20-FEB-2002

LOCUS
DEFINITION
AGENCOURT_6580965 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5469522

ACCESSION
VERSION
BM554590.1 GI:18794315

KEYWORDS
EST.

SOURCE
ORGANISM

human.
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 1089)
NIH-MGC <http://mgc.nhl.nih.gov/>.

AUTHORS
TITLE
JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DPF
cDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:

<http://image.lnl.gov>
Plate: LNCM1974 row: n column: 19

High quality sequence start: 4
High quality sequence stop: 684.

Location/Qualifiers
1..1089

/organism="Homo sapiens"
/db_xref="taxon:9606"

/clone="IMAGE:5469522"

/clone_id="NIH_MGC_41"

/tissue_type="amelanotic melanoma, cell line"

/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pORF7; site.1: XhoI; site.2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
SuperScript II RT (Life Technologies). Note: this is a
NIH_MGC library."

BASE COUNT 189 a 347 c 332 g 219 t 2 others
ORIGIN

Query Match 45.3%; Score 949.2; DB 13; Length 1089;
Best Local Similarity 96.3%; Pred. No. 3.8e-218;

Matches 1013; Conservative 0; Mismatches 35; Indels 4; Gaps 4;

1 CGCAGGACACCATGTGACCCCTGGTGAAGCTGGTGGCTTAAACAGACAGGGCTGGTGGCT 60
30 CGCAGGACACCATGTGACCCCTGGTGAAGCTGGTGGCTTAAACAGACAGGGCTGGTGGCT 89
61 GGAAGCGGCTGCGCCAGATGCTGATTTGCGCTTGGCTGCTGGTGAACCCCGAGAGA 120
90 GGAAGCGGCTGCGCCAGATGCTGATTTGCGCTTGGCTGCTGGTGAACCCCGAGAGA 149
121 GCGAGCTACAGTGGTGGCCCTGCTGGACAAATGGCCCAACACTGAGAGGCAT 180
150 GCGAGCTACAGTGGTGGCCCTGCTGGACAAATGGCCCAACACTGAGAGGCAT 209

QY	181	CTGGGTGGCCCCCTGGCAGGTGTGATCCCAAGCTCTGGCGGGCACATCCGATCTTTTACC	240
Db	210	CTGGGTGGCCCCCTGGCAGGTGTGATCCCAAGCTCTGGCGGGCACATCCGATCTTTTACC	269
QY	241	GTCTCAGGGACTTCCAGTTGCTGTCGCCCTTCCAGAGGCCGTGGCATGGGGGATGGCAAT	300
Db	270	GTCTCAGGGACTTCCAGTTGCTGTCGCCCTTCCAGAGGCCGTGGCATGGGGGATGGCAAT	329
QY	301	CACGTCTCCCAACGGGGGCTTGCATCTGCAGTGTGAGACGGGGCATTCCTGCTTCCAAAGATCA	360
Db	330	CACGTCTCCCAACGGGGGCTTGCATCTGCAGTGTGAGACGGGGCATTCCTGCTTCCAAAGATCA	389
QY	361	GGTAAACAATCCGTGGGTGCATCCAGTGGCCCTGATAGTTCAGTTGGAATGCCCCGACTTC	420
Db	390	GGTAAACAATCCGTGGGTGCATCCAGTGGCCCTGATAGTTCAGTTGGAATGCCCCGACTTC	449
QY	421	TCCACGTCTCTGTTATGTGCGATGGCTTCCTGGGGGTGCTGCCCATATGCCAGGCTTCC	480
Db	450	TCCACGTCTCTGTTATGTGCGATGGCTTCCTGGGGGTGCTGCCCATATGCCAGGCTTCC	509
QY	481	TGCATGTAAAGACAGGGGTGCACGTGCTCGGACGGGTGGCTTCTGGACCTGGTTTCACACC	540
Db	510	TGCATGTAAAGACAGGGGTGCACGTGCTCGGACGGGTGGCTTCTGGACCTGGTTTCACACC	569
QY	541	CGCTGCATCACACCACCGGACCCACCCCTCGGCAAAAGAAATCTCCCTGCCACAGAGACT	600
Db	570	CGCTGCATCACACCACCGGACCCACCCCTCGGCAAAAGAAATCTCCCTGCCACAGAGACT	629
QY	601	AACAGGGGAGTGGCTTTCACAGTCCGGTGCATAGTCTCCGGAGACAGTCCCGGTGCTCT	660
Db	630	AACAGGGGAGTGGCTTTCACAGTCCGGTGCATAGTCTCCGGAGACAGTCCCGGTGCTCT	689
QY	661	GATGGTTTACTGCTGCTGTGAGAGTGCACAGTGGGAATATAGCTGCTGCCCAATGCCCAAC	720
Db	690	GATGGTTTACTGCTGCTGTGAGAGTGCACAGTGGGAATATAGCTGCTGCCCAATGCCCAAC	749
QY	721	GCCACCTCTGCTCCGATACACTGCACTGTCTCCCCCAAGACACTGTGTCTACTCTGATC	780
Db	750	GCCACCTCTCTCCGATACACTGCACTGTCTCCCCCAAGACACTGTGTCTACTCTGATC	809
QY	781	CAGAGTAAGTCCCTTCCAAAGAGAACCTTACACAGGACCTCTCTACTTAAGTGGCTGGC	840
Db	810	CAGAGTAAGTCCCTTCCAAAGAGAACCTTACACAGGACCTCTCTACTTAAGTGGCTGGC	868
QY	841	CACACAGT - GGGCGATGTGAAATGTGACATGGAGGTGAGCTGCCACAGATGCTATACCTG	899
Db	869	CACACAGTGTGGGGGATGTGAAATGTGACATGGAGGTGAGCTGCCACAGATGCTATACCTG	928
QY	900	CTGGCGTCTAACAGT - GGGGGGCTGGGGGCTGTGGCCCTTTACCCAGGCTGTGTCTGTG	958
Db	929	CTGGCGTCTAACAGTGGGGGCTGTGGGGGCTGTGGCCCTTTTACCCAGGCTGTGTCTGTG	988
QY	959	AGGACACATACACTGCTGTCCCGGGGGTTTACGTGT - GACACGCAGAGGGTACTGT	1017
Db	989	AAGACACATACACTGCTGTCCCGGGGGTTTACGTGTGGAACCCAAAGGTTACTGTG	1048
QY	1018	GAACAGGGGGCCCCACAGGTGCTCTGGAATGA	1049
Db	1049	TGACAGGGGGCCCCACAGGGGGCCCCCTGGA	1080

RESULT	5
LOCUS	AL551350
DEFINITION	1033 bp mRNA linear EST, 16-FEB--2001 AL551350 LTL_NPTL006.PL2 Homo sapiens cDNA clone CSDDI0064YG14 5'
ACCESSION	prime; mRNA sequence.
VERSION	AL551350
KEYWORDS	AL551350.1 GI:12889213
SOURCE	EST,
ORGANISM	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	SOURCE
1 (bases 1 to 1033)	Li, W.B., Gruber, C., Jesssee, J. and Polayres, D.	Full-length cDNA libraries and normalization	Unpublished (2001)	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.	Location/Qualifiers	1. .1033 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="CSDD1064YG14" /clone_lib="Erl_NFL006_PL2" /clone_type="Placenta" /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-Oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

Query Match	45.0%: Score 943.6; DB 9; Length 1033;
Best Local Similarity	98.6%: Pred. No. 8.4e-217;
Matches 982; Conservative 1; Mismatches 10; Indels 3; Gaps 3;	
QY 1 CGCAGCGAGACCATGTGGACCCCTGGTGGACCGGGTGGCCCTTAAACAGCAGGGCTGGTGCT 60	
Db 38 CGCAGCGAGACCATGTGGACCCCTGGTGGACCGGGTGGCCCTTAAACAGCAGGGCTGGTGCT 97	
QY 61 GGAAGCGGGTGGCCAGATGGTCACTTCTGGCCCTGTGGCTGTGGCTGGACCCCGGAGGA 120	
Db 98 GGAAGCGGGTGGCCAGATGGTCACTTCTGGCCCTGTGGCTGTGGCTGGACCCCGGAGGA 157	
QY 121 GCCAGCTACAGTGTGGCGCGTCCCTTTGGACAATGGCCCAACAACCTGACAGGAGAT 180	
Db 158 GCCAGCTACAGTGTGGCGCGTCCCTTTGGACAATGGCCCAACAACCTGACAGGAGAT 217	
QY 181 CTGGTGGCCCCCTGGCAGATTGATGCCACACTGCTCTGCCGGCCACTCTCGACTTTTACC 240	
Db 218 CTGGTGGCCCCCTGGCAGATTGATGCCACACTGCTCTGCCGGCCACTCTCGACTTTTACC 277	
QY 241 GTCCTAGGAGACTTCAGATGGCTGCCCTTCCACAGAGGCGTGGCAATGGGGGATGGGCAT 300	
Db 278 GTCCTAGGAGACTTCAGATGGCTGCCCTTCCACAGAGGCGTGGCAATGGGGGATGGGCAT 337	
QY 301 CACTGCTGCCACAGGGGCTTCACATGCAGTGCAGAGGGGCGATTCCTGCTTCCAAAGATCA 360	
Db 338 CACTGCTGCCACAGGGGCTTCACATGCAGTGCAGAGGGGCGATTCCTGCTTCCAAAGATCA 397	
QY 361 GGTAACTACCTCGTGGGGGCGCATCCAGTGGCCCTGATAGCAATTTGGAATGCCCGACTTC 420	
Db 398 GGTAACTACCTCGTGGGGGCGCATCCAGTGGCCCTGATAGCAATTTGGAATGCCCGACTTC 457	
QY 421 TCCACGTGCTGTATTGGTGCATGGCTCTGGGGGGTGTGCCCATGGCCCGAGGCTTCC 480	
Db 458 TCCACGTGCTGTATTGGTGCATGGCTCTGGGGGGTGTGCCCATGGCCCGAGGCTTCC 517	
QY 481 TGCCTTGAAGACAGGGTGCACCTGCTGTCCGACGGTGCCTTCTGGGACCTGGTTACACCC 540	
Db 518 TGCCTTGAAGACAGGGTGCACCTGCTGTCCGACGGTGCCTTCTGGGACCTGGTTACACCC 577	
QY 541 CGCTCTATCACAC -CCAGGGGACCCACACCCCTGGCAAAAGATCTCCCTGCCACAGAGAC 599	
Db 578 CGCTCTATCACACACACAGGGGACCCACCCCTGGCAAAAGATCTCCCTGCCACAGAGAC 637	
QY 600 TAAACGGGCACTGGCCTTGTCCAGCTCGGATATGTCTCCGACGACAGGATCCCGGTGCC 659	

```

Db 638 TAAACAGGCGAGTGGCTTGTCCAGCTGCTGATGTGTCGGAGCGAGCGTCCCGGTGCC 697
Oy 660 TGAATGTTTACCTCTGCTGAGCTGCCAGTGGAGATGATGCTGCTGGCCAAATGCCNA 719
Db 698 TGAATGTTTACCTCTGCTGAGCTGCCAGTGGAGATGATGCTGCTGGCCAAATGCCNA 757
Oy 720 GCGCAGCTGCTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 779
Db 758 GCGCAGCTGCTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 817
Oy 780 CCAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 839
Db 818 CCAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 877
Oy 840 CCAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
Db 878 GCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 937
Oy 900 CTGCGCTTACAGTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 959
Db 938 CTGCGCTTACAGTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 996
Oy 960 GGACCAATACAGTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 995
Db 997 GGA-CACATACAGTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1031

```

```

RESULT 6
LOCUS AL542702 1010 bp mRNA linear EST 16-FEB-2001
DEFINITION AL542702 LTI_FL002_PL1 Homo sapiens cDNA clone CS0D011YC02 5 prime
, mRNA sequence.
ACCESSION AL542702
VERSION AL542702.1 GI:12875005
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1010)
AUTHORS Li, M.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Source
1. 1010
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D011YC02"
/clone_lib="LTI_FL002_PL1"
/lab_host="DH10B"
/note="Organ: Placenta; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@life.techn.com URL :
http://fulllength.invitrogen.com"

```

BASE COUNT 170 a 327 c 300 g 211 t 2 others

Query Match 44.3%; Score 928.4; DB 9; Length 1010;
 Best Local Similarity 99.3%; Pred. No. 3.8e-213;
 Matches 951; Conservative 2; Mismatches 3; Indels 2; Gaps 2;

Oy 1 CGCAGGCGAGCAGTGTGACCTGTGTGAGCTGGTGGCTTAACAGCAGGCGTGTGGCT 60

```

Db 54 CGCAGGCGAGCAGTGTGACCTGTGTGAGCTGGTGGCTTAACAGCAGGCGTGTGGCT 113
Oy 61 GGAACGGGTCGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
Db 114 GGAACGGGTCGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 173
Oy 121 GCGACCTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 174 GCGACCTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 233
Oy 181 CTGGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 234 CTGGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 293
Oy 241 GTCCTAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 294 GTCCTAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 353
Oy 301 CACTGCTGCCACGCGGCTTCCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 360
Db 354 CACTGCTGCCACGCGGCTTCCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 413
Oy 361 GGTAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 414 GGTAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
Oy 421 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 474 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533
Oy 481 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 534 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593
Oy 541 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 594 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 653
Oy 601 AACAGGCGAGTGGCTTGTCCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 660
Db 654 AACAGGCGAGTGGCTTGTCCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 713
Oy 661 GATGTTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 714 GATGTTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 773
Oy 721 GCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 774 GCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 832
Oy 781 CAGAGTAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 833 CAGAGTAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 892
Oy 841 CACACAG-TGGGCGATGTGAATGTGACATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 899
Db 893 CACACAGTGGGGGATGTGAATGTGACATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 952
Oy 900 CTGCGCTTACAGTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 957
Db 953 CTGCGCTTACAGTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1010

```

```

RESULT 7
LOCUS AL572883 1018 bp mRNA linear EST 16-FEB-2001
DEFINITION AL572883 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1034YC17 3
prime, mRNA sequence.
ACCESSION AL572883
VERSION AL572883.1 GI:12931579
KEYWORDS EST.
SOURCE human.

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1018)
AUTHORS Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1..1018
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1034YCI17"
/clone_1lb="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: PCMVSPORT 6; Site: 1. NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the PCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 199 a 306 c 331 g 172 t 10 others
ORIGIN

Query Match 43.8%; Score 918; DB 9; Length 1018;
Best Local Similarity 96.9%; Pred. No. 1.2e-210;
Matches 980; Conservative 7; Mismatches 19; Indels 5; Gaps 5;

QY 1055 CCCCACTACCTCAGCTCCAGCCACCAACCTTGAAGAGATGTCCTGATATA 1114
DB 1018 CCCCACTACCTCAGCTCCAGCCACCAACCTTGAAGAGATGTCCTGATATA 959
QY 1115 ATGTACAGAGCTGCTCCCTCCGATACCTGCTGCAACTCAGTCTGGGAGTGGGGCT 1174
DB 958 ATGTACAGAGCTGCTCCCTCCGATACCTGCTGCAACTCAGTCTGGGAGTGGGGCT 899
QY 1175 GCTGTCCATCCAGAGAGCTGTGCTGCTGCGACACACGACTGCTGCCACGAT 1234
DB 898 GCTGTCCATCCAGAGAGCTGTGCTGCTGCGACACACGACTGCTGCCACGAGGCT 839
QY 1235 ACACGTGTGATGAGGGGAGTGCAGAGGAGGAGGAGTGCAGGAGTGCAGTGCAGA 1294
DB 838 ACACGTGTGATGAGGGGAGTGCAGAGGAGGAGGAGTGCAGGAGTGCAGTGCAGA 779
QY 1295 AGATG-CCTGCCCCCGCGGCTTATCCACCCAGAGACATCGCTGTGACACGAC 1353
DB 778 AGATGCGCTGCGCGGGGCTTATCCACCCAGAGACATCGCTGTGACACGAC 719
QY 1354 A-CCAGCTCCCGGTGGGCGGAACCTGCTCCGAGCCAGGAGTGGAGTGGGCTGCTG 1412
DB 718 ACCCACTGCGCGGTGGGCGAGACCTGCTCCGAGCCTGCGAGTGGGAGTGGGCTGCTG 659
QY 1413 CCAGTTGCCCATGCTGTGTGCTGCGAGATGCGACGACTGCTGCCGGCTGGCTAC 1472
DB 658 CCAGTTGCCCATGCTGTGTGCTGCGAGATGCGACGACTGCTGCCGGCTGGCTAC 599
QY 1473 CTGCAACGTGAAGGCTGATCTGCGAGAGAGAGTGGTCTGCGCAGCTGCACTT 1532
DB 598 CTGCAACGTGAAGGCTGATCTGCGAGAGAGAGTGGTCTGCGCAGCTGCACTT 539
QY 1533 CTTGGCCCGTGAAGCTGCTGCTGGAAGAGCTGAGTGTGGGAGAGACACTTCTG 1592
DB 538 CTTGGCCCGTGAAGCTGCTGCTGGAAGAGCTGAGTGTGGGAGAGASACTTCTG 479
QY 1593 CCATGATTAACGACCTGCTGCGAGACCAACGAGGGTGGGCTGCTCCCTACGC 1652
ORIGIN

DB 478 CCATGATTAACGACCTGCTGCGAGACCAACGAGGGTGGGCTGCTCCCTACGC 419
QY 1653 CCAAGGCGCTGTGTGCTGATGCGGCGCCACCTGCTGCTGCTGCTGCGGAGCAG 1712
DB 418 CCAAGGCGCTGTGTGCTGATGCGGCGCCACCTGCTGCTGCTGCTGCGGAGCAG 359
QY 1713 CAGGGGTACCAAGTGTGTGCGAGAGAGGCCCGCGCTGGAGGCCCTTTGAGAGACC 1772
DB 358 CAGGGGTACCAAGTGTGTGCGAGAGAGGCCCGCGCTGGAGGCCCTTTGAGAGACC 299
QY 1773 AGCCTTGAGACAGCTGCTGAGAGGAGACAGTGAAGTCTGACGCCCTGGAGCCCCA 1832
DB 298 AGCCTTGAGACAGCTGCTGAGAGGAGACAGTGAAGTCTGACGCCCTGGAGCCCCA 239
QY 1833 CTGAGAGGAGGCCCTGCTGCTGAGAGGCCCTGCTGAGAGGCCCTGAGAGGCCCTTCC 1892
DB 238 CTGAGAGGAGGCCCTGCTGCTGAGAGGCCCTGCTGAGAGGCCCTGAGAGGCCCTTCC 179
QY 1893 GACCCCATTTGAGACTCCCATCATCATCATCATCATCATCATCATCATCATCATCAT 1952
DB 178 GACCCCATTTGAGACTCCCATCATCATCATCATCATCATCATCATCATCATCATCAT 120
QY 1953 TGTGAGAGAGGGGTTGAGGAGAAAGC-CCATTAACAGCTGCCATCCCTCCGCTTACG 2011
DB 119 TGTGAGAGAGGGGTTGAGGAGAAAGCAGTGAAGTCTGAGAGGCCCTGAGAGGCCCTTACG 60
QY 2012 TGGACCTGTGAGGAGGCTGCTTTCCTATCA-CAGGGGTGTTGTGTGT 2061
DB 59 TGGACCTGTGAGGAGGCTGCTTTCCTATCA-CAGGGGTGTTGTGTGT 9

RESULT 8
AL561424 932 bp mRNA linear EST 16-FEB-2001
LOCUS AL561424
DEFINITION AL561424 LTI_NFL010_BC2 Homo sapiens cDNA clone CS0D1007Y12 5
prime, mRNA sequence.
ACCESSION AL561424
VERSION AL561424.1 GI:12908842
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 932)
AUTHORS Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1..932
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1007Y12"
/clone_1lb="LTI_NFL010_BC2"
/sex="male"
/tissue_type="B cells from Burkitt lymphoma"
/note="Vector: PCMVSPORT 6; Site: 1. NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the PCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 160 a 305 c 277 g 189 t 1 others
ORIGIN

Query Match 43.6%; Score 914; DB 9; Length 932;

Best Local Similarity 99.7%; Pred. No. 1.le-209;
Matches 925; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

```

OY 1 GCAGGCAACCATGATGGAGCCCTGGGAGCTGGGCTTAAACAGACAGGGGCTGGCT 60
    |||
DB 6 CCAGGCAACCATGATGGAGCCCTGGGAGCTGGGCTTAAACAGACAGGGGCTGGCT 65
OY 61 GGAAGCGGCTGGCCAGATAGTTCAGTTCGCTCCGCTGCTGCTGAGCCCGAGGA 120
    |||
DB 66 GGAAGCGGCTGGCCAGATAGTTCAGTTCGCTCCGCTGCTGCTGAGCCCGAGGA 125
OY 121 GCCAGCTAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
    |||
DB 126 GCCAGCTAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 185
OY 181 CTGGGCTGGCCCTGGCCAGCTGATGATGATGATGATGATGATGATGATGATGAT 240
    |||
DB 186 CTGGGCTGGCCCTGGCCAGCTGATGATGATGATGATGATGATGATGATGATGAT 245
OY 241 GTCTGAGGACCTTCAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
    |||
DB 246 GTCTGAGGACCTTCAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305
OY 301 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
    |||
DB 306 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 365
OY 361 GGTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
    |||
DB 366 GGTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 425
OY 421 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
    |||
DB 426 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 485
OY 481 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
    |||
DB 486 TCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 545
OY 541 CCCTGATACACACACACACACACACACACACACACACACACACACACACACACAC 600
    |||
DB 546 CCCTGATACACACACACACACACACACACACACACACACACACACACACACACAC 605
OY 601 AACAGGCGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
    |||
DB 606 AACAGGCGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 665
OY 661 GATGGTTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
    |||
DB 666 GATGGTTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 725
OY 721 GCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
    |||
DB 726 GCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 785
OY 781 CAGAGTAAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
    |||
DB 786 CAGAGTAAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 845
OY 841 CACACAGTGGGAGTGGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
    |||
DB 846 CACACAGTGGGAGTGGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 904
OY 901 TCCGCTTCACAGTGGGAGTGGTGGGCT 928
    |||
DB 905 TCCGCTTCACAGTGGGAGTGGTGGGCT 932

```

RESULT 9
AL582634/ 996 bp mRNA linear EST 16-FEB-2001
LOCUS AL582634 LTI_NFL010.BC2 Homo sapiens cDNA clone CS0DL007YF12 3
DEFINITION prime, mRNA sequence.

ACCESSION AL582634
VERSION AL582634.1 GI:12950809
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 996)
AUTHORS Li, W.B., Gruber, C., Jessup, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Séquençage
BP 191 91006 Evry cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. 996
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DL007YF12"
/clone_lib="LTI_NFL010_BC2"
/sex="male"
/issue_type="B cells from Burkitt lymphoma"
/note="Vector: pCMVSPORT 6; Site: L: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: filang@lifetech.com URL: <http://fulllength.invitrogen.com>"

BASE COUNT 199 a 299 c 320 g 171 t 7 others
ORIGIN

Query Match 43.2%; Score 904; DB 9; Length 996;
Best Local Similarity 96.9%; Pred. No. 2.9e-207;
Matches 957; Conservative 5; Mismatches 22; Indels 4; Gaps 4;

```

OY 1069 AGCTGCCAGACCCCAAGCCTTGAAGAGATGTCCTGGATTAATGACAGCTGT 1128
    |||
DB 996 AGCTGCCAGACCCCAAGCCTTGAAGAGATGTCCTGGATTAATGACAGCTGT 937
OY 1129 CCCTCTCCGATACCTGCTGCCACTCACTGTGGGAGTGGGCTGCTGCTCAATCCCA 1188
    |||
DB 936 CCCTCTCCGATACCTGCTGCCACTCACTGTGGGAGT -GGGCTGCTGCTCAATCCCA 878
OY 1189 GAGGCTGTCTGCTGCTGGACACGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCT 1248
    |||
DB 877 GAGGCTGTCTGCTGCTGGACACGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
OY 1249 GAGGCGAGTGCACGAGGAGGAGATGCTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 1308
    |||
DB 817 GAGGCGAGTGCACGAGGAGGAGATGCTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 759
OY 1309 CGCGTCTCTTATCCACCCCAAGACATCGGCTGTGACACAGACAGCAGTGGCTG 1368
    |||
DB 758 CGGCTCTCTTATCCACCCCAAGACATCGGCTGTGACACAGACACACAGTGGCTG 699
OY 1369 GCGGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1428
    |||
DB 698 GCGGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 639
OY 1429 GTCTCTGCGAGGATGCGCAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1488
    |||
DB 638 GTCTCTGCGAGGATGCGCAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 579
OY 1489 CGATCTCGAGAGAGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1548
    |||
DB 578 CGATCTCGAGAGAGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 519
OY 1549 CACGTGGTGTGAAGAGAGTGTGGGGAAGACACTTCTGCCATGATTAACAGACC 1608

```

|||||
Db 518 CACGGGGTGTGAAGAGCTGAGTGTGGGGAAGACACTTCTGCATGATTAACAGAAC 459
Oy 1609 TGTCTCCAGAGAACCCAGAGGGCTGGGCTGTCTCCCTACGAGGGCTGTCTGTGT 1668
|||||
Db 458 TGTCTCCAGAGAACCCAGAGGGCTGGGCTGTCTCCCTACGAGGGCTGTCTGTGT 399
Oy 1669 GCTGATCGGGCCACTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1728
Db 398 GCTGATCGGGCCACTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 339
Oy 1729 TTGGCAGAGGAGGG 1788
Db 338 TTGGCAGAGGAGGG 279
Oy 1789 CTGTGAGGAGACAGTACTGTAAGACTGTGAGCCCTGCGGACCCCACTCGAGGGTCCCTC 1848
Db 278 CTGTGAGGAGACAGTACTGTAAGACTGTGAGCCCTGCGGACCCCACTCGAGGGTCCCTC 219
Oy 1849 TGTCTAGGCTCCCTAGACACTCCCTTACCAAAATCTCCCTGAGACCCCACTTGTAGCT 1908
Db 218 TGTCTAGGCTCCCTAGACACTCCCTTACCAAAATCTCCCTGAGACCCCACTTGTAGCT 159
Oy 1909 CCCCATCAACATGGAGAGTGGGGGCTCAATCTAAGCCCTTCCCTGTAGAGAGGGGGTGG 1968
Db 158 CCCCATCAACATGGAGAGTGGGGGCTCAATCTAAGG-CCTTCCCTGTAGAGAGGGGGTGG 100
Oy 1969 AGGCAAAAGCC-CATTACAAGCTGCAATCCCTCCCGTTTCAGTGAAGACCTGTGGCCAG 2027
Db 99 TGGCAAAAGCCATTAACAAGCTGCCATCCCTCCCGTTTCAGTGAAGACCTGTGGCCAG 40
Oy 2028 GTGCTTTTCCCTATCCACAGGGGGTGT 2055
Db 39 GTGCTTTTCCCTATCCACAGGGGGTGT 12
RESULT 10
AL541798 934 bp mRNA linear EST 16-FEB-2001
LOCUS AL541798 LTI_FL002_P11 Homo sapiens cDNA clone CS0DE007Y118 5 prime
DEFINITION mRNA sequence.
ACCESSION AL541798
VERSION AL541798.1 GI:12873213
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 934)
AUTHORS Li, W.B., Gruber, C., Jessup, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.
FEATURES
source
1..934
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DE007Y118"
/clone_11b="LTI_FL002_P11"
/lab_host="DH10B"
/note="Organ: Placenta; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by life
technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 170 a 295 c 284 g 180 t 5 others
ORIGIN
Query Match 43.0%; Score 901.8; DB 9; Length 934;
Best Local Similarity 98.1%; Pred. No. 9.7e-207;
Matches 917; Conservative 5; Mismatches 12; Indels 1; Gaps 1;
Oy 581 ACCTCCCTGCCAGAGAGACTTAACAGGGAGTGGCTGTGTCAGCTCGGTGATGTCCGG 640
Db 1 ACCTCCCTGCCAGAGAGACTTAACAGGGAGTGGCTGTGTCAGCTCGGTGATGTCCGG 60
Oy 641 AGCAGAGTCCCGGTGGTCCCTGATGGTTCACCTGCTGTAGCTGCCAGTGGGAAGTATG 700
Db 61 AGCAGAGTCCCGGTGGTCCCTGATGGTTCACCTGCTGTAGCTGCCAGTGGGAAGTATG 120
Oy 701 GCTGTGCCCAATGCCCAAGGCCACCTGTGCTGCCATCACTGTGACACTGACCTGCCCAAG 760
Db 121 GCTGTGCCCAATGCCCAAGGCCACCTGTGCTGCCATCACTGTGACACTGACCTGCCCAAG 180
Oy 761 ACAGTGTGTGACCTGATCCAGAGTAACTGCTCTCCAAAGAGAAAGCTACAGGAGC 820
Db 181 ACAGTGTGTGACCTGATCCAGAGTAACTGCTCTCCAAAGAGAAAGCTACAGGAGC 240
Oy 821 TCTCACTAAGCTGCTGCTGGCAGACAGTGGCGATGTGAATGTGACATGAGGTAGCT 880
Db 241 TCTCACTAAGCTGCTGCTGGCAGACAGTGGCGATGTGAATGTGACATGAGGTAGCT 300
Oy 881 GCCCAGATGGCTATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 940
Db 301 GCCCAGATGGCTATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Oy 941 CCCAGAGTGTGTGCTGTGAGGACCAATACACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1000
Db 361 CCCAGAGTGTGTGCTGTGAGGACCAATACACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Oy 1001 CGCAGAGGGGTACCTGTGTAACAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1060
Db 421 CGCAGAGGGGTACCTGTGTAACAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 480
Oy 1061 CTCACCTCAGCTGCGCAGACCCCAAGCCTTGAAGAGATGCTCCCTGTGTAATGTCA 1120
Db 481 CTCACCTCAGCTGCGCAGACCCCAAGCCTTGAAGAGATGCTCCCTGTGTAATGTCA 540
Oy 1121 GCAGCTGTCCCTCTCCGATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1180
Db 541 GCAGCTGTCCCTCTCCGATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Oy 1181 CAATCCCAAGGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1240
Db 601 CAATCCCAAGGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Oy 1241 GTGTAGCTGAGGGGAGCTGTGACAGGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1300
Db 661 GTGTAGCTGAGGGGAGCTGTGACAGGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Oy 1301 CTGCGCGCGGGGTCTCTATCCACCAGACATCGGCTGTGACAGACACACAGCT 1360
Db 721 CTGCGCGCGG-GCTTCTCTATCCACCAGACATCGGCTGTGACAGACACACAGCT 779
Oy 1361 GCCCGGTGGGGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1420
Db 780 GCCCGGTGGGGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 839
Oy 1421 CCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1480
Db 840 CCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
Oy 1481 TGAAGGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1515
Db 900 TGAAGGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 934
RESULT 11

[illegible]

Db	458	TCACAGTGCCTGTGTTATGTATGGTGGATGGCGTCTGGGGGTCTGCCCATATGCCCAGGCTTCC	517
QY	481	TGCTGTGAAGCAGGGGTGCACGTGCTGTCCGACAGGTGCTTCTGTGGACCTGGTTCCACAC	540
Db	518	TGCTGTGAAGACAGGGGTGCACGTGCTGTCCGACAGGTGCTTCTGTGGACCTGGTTCCACAC	577
QY	541	CGCTGCATCACACCCACGGGACCCACCCCTTGGCMAAAGATCCCTTGCCACAGAGACT	600
Db	578	CGCTGCATCACACCCACGGGACCCACCCCTTGGCMAAAGATCCCTTGCCACAGAGACT	637
QY	601	AACAGGCGATGGCCCTTGTCCAGCTCGGTCAATGTGTCCGAGCAGCAGGTCCCGGTGCCCT	660
Db	638	AACAGGCGATGGCCCTTGTCCAGCTCGGTCAATGTGTCCGAGCAGCAGGTCCCGGTGCCCT	697
QY	661	GATGTTTACTGCTGTGTGAGCTGCCCAGTGGGAAGTATGGCTGCTGCCCAATGCCCAAC	720
Db	698	GATGTTTACTGCTGTGTGAGCTGCCCAGTGGGAAGTATGGCTGCTGCCCAATGCCCAAC	757
QY	721	GCCACCTCTCTCTCCGATCACCCTGCATGCTGCTGCTGCCCAAGACACTGTGTGTGACTGTATC	780
Db	758	GCCACCTCTCTCTCCGATCACCCTGCATGCTGCTGCTGCCCAAGACACTGTGTGTGACTGTATC	817
QY	781	CAGAGTAGTGCCCTTCCAAAGAGAACCTACACAGGACCTCCACATTAAGCTGCTTCGG	840
Db	818	CAGAGTAGTGCCCTTCCAAAGAGAACCTTMCACAGGACCTCCACATTAAGCTGCTTCGG	877
QY	841	CACACAGTGGGCGATGTGAAATGTGACATGAGAGGTGACTGTC	883
Db	878	CACACAGTGGGCGATGTGAAATGTGAAATGTGAGAGGTGACTGTC	920

FEATURES	Source
REFERENCE	AL542659 942 bp mRNA linear EST 16-FEB-2001
AUTHORS	AL542659 LTI_FL002_PL1 Homo sapiens CDNA clone CS0DE014YB02 5 prime
TITLE	1 (bases 1 to 942)
JOURNAL	Full-length cDNA libraries and normalization
COMMENT	Unpublished (2001)
	Contact: Genoscope
	Genoscope - Centre National de Sequencage
	BP 191 91006 Evry cedex - France
	Email: seqre@genoscope.cns.fr, Web : www.genoscope.cns.fr.
	Location/Qualifiers
	1. 942
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="CS0DE014YB02"
	/clone_1lb="LTI_FL002_PL1"
	/lab_host="DH10B"
	/note="Organ: placenta; Vector: PCWSPORT 6; 1st strand
	cDNA was primed with a NotI-oligo(dT) primer. Five prime
	end enriched, double-stranded cDNA was digested with Not I
	and cloned into the Not I and Eco RV sites of the
	PCWSPORT 6 vector. Library was constructed by life
	Technologies. Contact : Feng Liang life Technologies, a
	division of Invitrogen 9800 Medical Center Drive Rockville
	, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
	li.fang@lifestech.com URL :
	http://fulllength.invitrogen.com"
BASE COUNT	165 a 311 c 287 g 176 t 3 others
ORIGIN	
Query Match	41.7% Score 873.8; DB 9; Length 942;
Best Local Similarity	97.8% Pred. No. 5.5e-200;

Db 489 TCGCTTGAAAGACAGGGTGCATGCTGCTCCGACAGGTGCTTGGACACTGTTTCACACC 548
Oy 541 CGCTGCATACACACCCAGGGGACACCCCTTGGCAAGAGTCCCTGCGCAGAGACT 600
Db 549 CGGTGATACACACCCAGGGGACACCCCTTGGCAAGAGTCCCTGCGCAGAGACT 608
Oy 601 AACAGGGCAGTGGCCCTTTGTCACAGCTGGTCAATGTGTCGGAGCCAGGTTCCGGTCCCT 660
Db 609 AACAGGGCAGTGGCCCTTTGTCACAGCTGGTCAATGTGTCGGAGCCAGGTTCCGGTCCCT 668
Oy 661 GATGTTTACACTGCTGTGAGTGGCCAGTGGGAGTATGGGCTGGCCCAATGGCCCAAC 720
Db 669 GATGTTTACACTGCTGTGAGTGGCCAGTGGGAGTATGGGCTGGCCCAATGGCCCAAC 728
Oy 721 GCCACCTGCTGCTCCGATACCTGACCTGCTGCCCCCAAGACACTGTGTGTGACCTGATC 780
Db 729 GCCACCTGCTGCTCCGATACCTGACCTGCTGCCCCCAAGACACTGTGTGTGACCTGATC 788
Oy 781 CAGAGTAAGTGGCTTCCCAAGGAGAACGCTACAGGAGCTCTCACTAAGCTGCTGCC 840
Db 789 CAGAGTAAGTGGCTTCCCAAGGAGAACGCTACAGGAGCTCTCACTAAGCTGCTGCC 848
Oy 841 CACACAGT-GGGGAGTGTGAATGTGACATGGAGTGGAGTGGCCCA 885
Db 849 CACACAGTGGGGAGTGTGAATGTGACATGGAGTGGAGTGGCCCA 894

RESULT 14
AL544054 888 bp mRNA linear EST 16-FEB-2001
LOCUS AL544054 LTI_NFL006_PL2 Homo sapiens cDNA clone CSOD1004YH24 5
DEFINITION prime, mRNA sequence.
ACCESSION AL544054
VERSION AL544054.1 GI:12876533
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source 1..888
Location/Qualifiers
1..888
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSOD1004YH24"
/clone_1lb="LTI_NFL006_PL2"
/tissue_type="Placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
life technologies. Contact: Feng Liang life technologies,
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@life.techn.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 155 a 269 c 255 g 181 t 28 others
ORIGIN

Query Match 40.8%; Score 854.4; DB 9; length 888;
Best Local Similarity 96.3%; Pred. No. 2.6e-195;
Matches 854; Conservative 23; Mismatches 9; Indels 1; Gaps 1;
Oy 26 TGAGCTGGGTGGCTTAACAGCAGGGGCTGTGGTGAACGGGTCGCCAGATGTGCACT 85
|||||

Db 1 TGAGCTGGGTGGCTTAACAGCAGGGGCTGTGGTGAACGGGTCGCCAGATGTGCACT 60
Oy 86 TGTGCCCTGTGGCTGTGCTGTGAGACCCGAGAGACAGCTACAGCTGTGCTGCCGCCC 145
Db 61 TGTGCCCTGTGGCTGTGCTGTGAGACCCGAGAGACAGCTACAGCTGTGCTGCCGCCC 120
Oy 146 TTTGTGACAATATGGCCACACACTGAGCAGAGCATCTGGGTGGCCCTGCCAGTTGATG 205
Db 121 TTTGTGACAATATGGCCACACACTGAGCAGAGCATCTGGGTGGCCCTGCCAGTTGATG 180
Oy 206 CCCACGTCTGTGGCCGACCTCTGATCTTTACCTCTCAGAGGATTTCCATTTGTGTGTC 265
Db 181 CCCACGTCTGTGGCCGACCTCTGATCTTTACCTCTCAGAGGATTTCCATTTGTGTGTC 240
Oy 266 CTTTCCCAAGGCGTGGATGCGGGATGGCCATGATGCTGCCACGAGGCTTCCACT 325
Db 241 CTTTCCCAAGGCGTGGATGCGGGATGGCCATGATGCTGCCACGAGGCTTCCACT 300
Oy 326 GCAGTGCACAGGGGCGATCTGCTTCCAAAGATCAGTAAACAATCTCGTGGTCCATCC 385
Db 301 GCAGTGCACAGGGGCGATCTGCTTCCAAAGATCAGTAAACAATCTCGTGGTCCATCC 360
Oy 386 AGTGGCTGATATGTCAGTTCGAAATGCGCGGACTTCTCCACAGTGTGTATATGTGATG 445
Db 361 AGTGGCTGATATGTCAGTTCGAAATGCGCGGACTTCTCCACAGTGTGTATATGTGATG 420
Oy 446 GCTCTGTGGGGGTGCTGCTGCCATGCGCCAGAGCTTCTGCTGTGAAGACAGAGTGCATGCT 505
Db 421 GCTCTGTGGGGGTGCTGCTGCCATGCGCCAGAGCTTCTGCTGTGAAGACAGAGTGCATGCT 480
Oy 506 GTCCGACAGGCTGCTTGTGCGACCTGCTTACACACCCGTCATACACCCAGGCGACCC 565
Db 481 GTCCGACAGGCTGCTTGTGCGACCTGCTTACACACCCGTCATACACCCAGGCGACCC 540
Oy 566 ACCCCCTGGCAAGAGCTCCCTGCGCCAGAGACTTACAGAGGCGAGTGGCTGTCCAGCT 625
Db 541 ACCCCCTGGCAAGAGCTCCCTGCGCCAGAGACTTACAGAGGCGAGTGGCTGTCCAGCT 600
Oy 626 CGGTCAATGTGTCCGAGCAGGATCCCGGTGCGCTGATGTTCTACCTGCTGTGAGCTGC 685
Db 601 CGGTCAATGTGTCCGAGCAGGATCCCGGTGCGCTGATGTTCTACCTGCTGTGAGCTGC 660
Oy 686 CCAGTGGGAATATGCTGCTGCTGCCAATGCCCAACGCCACCTGTGCTCCGATCACTGC 745
Db 661 CCAGTGGGAATATGCTGCTGCTGCCAATGCCCAACGCCACCTGTGCTCCGATCACTGC 720
Oy 746 ACTGCTGCCCCCAAGCAGCTGTGTGAGCTGTGATCCAGATGAAGTCCCTCCAAAGGAGA 805
Db 721 ACTGCTGCCCCCAAGCAGCTGTGTGAGCTGTGATCCAGATGAAGTCCCTCCAAAGGAGA 780
Oy 806 AGCTACACAGGACCTCTCACTAAGCTCCTGCGCACACAGT-GGGCAGTGTGAATGT 864
Db 781 AGCTACACAGGACCTCTCACTAAGCTCCTGCGCACACAGTGTGAATGT 840
Oy 865 GACATGAGGTGAGCTGCCAGATGAGCTTATACCTGCTGCCGTCTACA 911
Db 841 GACATGAGGTGAGCTGCCAGATGAGCTTATACCTGCTGCCGTCTACA 887

RESULT 15
BM468251 991 bp mRNA linear EST 05-FEB-2002
LOCUS BM468251 AGENCOURT_6475640 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5578048
DEFINITION 5', mRNA sequence.
ACCESSION BM468251
VERSION BM468251.1 GI:18517293
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS NIH-MGC http://mgi.mgi.nhl.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strassberg, Ph.D.
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCMD/MP
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
Cloned Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLNL12332 row: h column: 17
High quality sequence stop: 670.

FEATURES
source
1. .991
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5578048"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1; Note:
Site: 2; Salt: Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

BASE COUNT 170 a 325 c 295 g 201 t
ORIGIN

Query Match 40.5%; Score 849; DB 13; Length 991;
Best Local Similarity 96.1%; Pred. No. 5.3e-194;
Matches 904; Conservative 0; Mismatches 30; Indels 7; Gaps 3;

QY 1 CGCAGGACAGACATGAGACCTGTGAGCTGGGTGACCTTAACAGCAGGGCTGTGGCT 60
DB 13 CGCAGGACAGACATGAGACCTGTGAGCTGGGTGACCTTAACAGCAGGGCTGTGGCT 72
QY 61 GGAACGGGGTCCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 73 GGAACGGGGTCCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 132
QY 121 GCCAGCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 133 GCCAGCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 192
QY 181 CTGGGTGGCCCTGCCAGCTTGTATGCCACACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 193 CTGGGTGGCCCTGCCAGCTTGTATGCCACACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 252
QY 241 GTCTCAGGAGCTTCCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 253 GTCTCAGGAGCTTCCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 312
QY 301 CACTGGTGGCCAGGGGGCTTCCACTGAGTGCAGAGGGGGGATGCTGCTGCTGCTGCTGCTGCT 360
DB 313 CACTGGTGGCCAGGGGGCTTCCACTGAGTGCAGAGGGGGGATGCTGCTGCTGCTGCTGCTGCT 372
QY 361 GGTAACTCCGTGGGTGCCATCCAGTGCCTGATAGTGAATGCAATGCCGAGCTTC 420
DB 373 GGTAACTCCGTGGGTGCCATCCAGTGCCTGATAGTGAATGCAATGCCGAGCTTC 432
QY 421 TCCAGCTGCTGTATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 433 TCCAGCTGCTGTATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 492
QY 481 TGGGTGAAGAGAGGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 493 TGGGTGAAGAGAGGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 552
QY 541 CGCTGATCAACACCAAGGGGACCCCTGCAAGAAAGCTCCCTGCCAGAGGACT 600
DB 553 CGCTGATCAACACCAAGGGGACCCCTGCAAGAAAGCTCCCTGCCAGAGGACT 612
QY 601 AACAGGGCACTGGCTTGTCCAGCTGGGTCAATGCTCCGAGCAGCAGGTCGCCGCT 660

DB 613 AACAGGGCACTGGCTTGTCCAGCTGGGTCAATGCTCCGAGCAGCAGGTCGCCGCT 672
QY 661 GATGTTCTACCTGCTGTGAGCTGCCAGTGGGAAATGATGCTGCTGCTGCTGCTGCTGCT 720
DB 673 GATGTTCTACCTGCTGTGAGCTGCCAGTGGGAAATGATGCTGCTGCTGCTGCTGCTGCT 732
QY 721 GCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 733 GCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792
QY 781 CAGAGTAAGTCCCTCTCCAAAGAGAACGCTAACAC-GGACCTCTCTAAGTGGCTGC 839
DB 793 CAGAGTAAGTCCCTCTCCAAAGAGAACGCTAACACGCGGACCTCTCTAAGTGGCTGC 852
QY 840 GCACAGATGGGGG---ATGTGAATGTGACATGAGGTGAGCGGCCAGATGGC---TA 893
DB 853 GCACAGATGGGGGAGATGTAAATGTGAACATGAGGTGAGCTGCCCCAAATGCTTAA 912
QY 894 TACCTGCTGCTGCTTACAGTCCGGGGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 934
DB 913 ACCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 953

Search completed: February 21, 2003, 15:20:29
Job time : 2734 secs

THIS PAGE BLANK (USPTO)